

OM protein - protein search, using sw model

Run on: January 24, 2005, 21:27:49 ; Search time 106.921 Seconds
(without alignments)
1207.832 Million cell updates/sec

Title: US-10-791-166-4
Perfect score: 1900
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVSTSTNPSTGQEVSAGL 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1900	100.0	360	2	AAR79166	Aar79166 Human mon
2	1900	100.0	360	2	AAW35833	Aaw35833 Human mon
3	1900	100.0	360	4	AAG80108	Aag80108 Human CCR
4	1900	100.0	360	4	AAU07614	Aau07614 Human wil
5	1900	100.0	360	6	ABP97725	Abp97725 Amino aci
6	1900	100.0	360	6	ABP81987	Abp81987 Human C-C
7	1900	100.0	360	8	ADM67225	Adm67225 Human adi
8	1900	100.0	360	8	ADL82831	Adl82831 Human PRO
9	1899	99.9	360	4	AAU07613	Aau07613 Human CCR

10	1894	99.7	360	4	ABB56340	Abb56340	Non-endog
11	1838	96.7	347	7	ADF56627	Adf56627	Partial h
12	1651.5	86.9	374	2	AAR79165	Aar79165	Human mon
13	1651.5	86.9	374	4	AAG80107	Aag80107	Human CCR
14	1651.5	86.9	374	6	ABU09083	Abu09083	Human che
15	1651.5	86.9	374	7	ADD44861	Add44861	Human Pro
16	1651.5	86.9	374	7	ADD44865	Add44865	Human Pro
17	1651.5	86.9	374	7	ADP65146	Adp65146	Human che
18	1651.5	86.9	374	8	ADO29221	Ado29221	Human GPC
19	1568.5	82.6	344	5	ABG92881	Abg92881	Class I r
20	1568.5	82.6	344	6	ABU61655	Abu61655	Human mon
21	1568.5	82.6	344	7	ADF72129	Adf72129	Human G-p
22	1568.5	82.6	344	8	ADP86217	Adp86217	Human MCP
23	1535	80.8	373	8	ADM67224	Adm67224	Murine ad
24	1535	80.8	373	8	ADO29222	Ado29222	Mouse GPC
25	1535	80.8	373	8	ADP74040	Adp74040	Murine CC
26	1473	77.5	329	4	AAB46859	Aab46859	Human MCP
27	1473	77.5	329	5	ABB81055	Abb81055	Human MCP
28	1396	73.5	354	8	ADO29228	Ado29228	Mouse GPC
29	1386	72.9	354	2	AAW54037	Aaw54037	Mouse CC-
30	1386	72.9	354	7	ADD44859	Add44859	Rat Prote
31	1386	72.9	354	7	ADD44863	Add44863	Rat Prote
32	1371	72.2	352	4	AAG79089	Aag79089	Amino aci
33	1364	71.8	352	2	AAW27407	Aaw27407	Human CCR
34	1364	71.8	352	2	AAW27123	Aaw27123	Human che
35	1364	71.8	352	2	AAW27125	Aaw27125	Macaque c
36	1364	71.8	352	2	AAW23835	Aaw23835	Human CC
37	1364	71.8	352	2	AAW88232	Aaw88232	HIV-1 co-
38	1364	71.8	352	4	AAG80111	Aag80111	Human CCR
39	1364	71.8	352	4	AAE04321	Aae04321	Human che
40	1364	71.8	352	4	AAB83354	Aab83354	Human CCR
41	1364	71.8	352	4	AAB82948	Aab82948	Human HIV
42	1364	71.8	352	5	AAM52828	Aam52828	Human CC
43	1364	71.8	352	5	ABB08343	Abb08343	Human che
44	1364	71.8	352	6	ABR58602	Abr58602	Human can
45	1364	71.8	352	6	AAO29514	Aao29514	Human C-C

ALIGNMENTS

RESULT 1

AAR79166

ID AAR79166 standard; protein; 360 AA.

XX

AC AAR79166;

XX

DT 25-MAR-2003 (revised)

DT 29-DEC-1995 (first entry)

XX

DE Human monocyte chemoattractant protein-1 receptor MCP-1RB.

XX

KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1. .48
 FT /label= extracellular
 FT Domain 49. .70
 FT /label= transmembrane
 FT Domain 80. .700
 FT /label= transmembrane
 FT Domain 115. .136
 FT /label= transmembrane
 FT Domain 154. .178
 FT /label= transmembrane
 FT Domain 204. .231
 FT /label= transmembrane
 FT Domain 244. .268
 FT /label= transmembrane
 FT Domain 295. .313
 FT /label= transmembrane
 FT Region 314. .360
 FT /label= carboxyl tail
 XX
 PN WO9519436-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 11-JAN-1995; 95WO-US000476.
 XX
 PR 13-JAN-1994; 94US-00182962.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Charo I, Coughlin S;
 XX
 DR WPI; 1995-263866/34.
 DR N-PSDB; AAQ96298.
 XX
 PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocytic infiltrates.
 XX
 PS Claim 2; Fig 2; 84pp; English.
 XX
 CC To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
 CC HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pFROG and probed with the PCR product. A 2.1
 CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC sequence first obtd. from the 5' UTR through the putative seventh
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxyl
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-

CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.8e-206;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL	360
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL	360

RESULT 2

AAW35833

ID AAW35833 standard; protein; 360 AA.

XX

AC AAW35833;

XX

DT 27-FEB-1998 (first entry)

XX

DE Human monocyte chemoattractant protein 1 receptor.

XX

KW Human; MCP-1; monocyte chemoattractant protein; receptor; tumour;

KW inflammatory disease; viral; allergy; diabetes.

XX

OS Homo sapiens.

XX

PN JP09238688-A.

XX

PD 16-SEP-1997.

XX

PF 11-MAR-1996; 96JP-00053574.

XX

PR 11-MAR-1996; 96JP-00053574.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1997-506557/47.
 DR N-PSDB; AAT96976.
 XX
 PT DNA encoding human monocyte chemoattractant protein 1 receptor - used to
 PT treat tumours and inflammatory, viral, infectious, allergic, diabetic and
 PT central nervous system diseases.
 XX
 PS Disclosure; Page 12-14; 15pp; Japanese.
 XX
 CC The present sequence represents human monocyte chemoattractant protein 1
 CC (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA are
 CC used for the prevention and treatment of tumours and inflammatory, viral,
 CC infectious, allergic, diabetic and central nervous system diseases
 XX
 SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.8e-206;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTDIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTDIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360

RESULT 3

AAG80108

ID AAG80108 standard; protein; 360 AA.

XX

AC AAG80108;

XX

DT 17-JAN-2002 (first entry)

XX

DE Human CCR2b protein.

XX
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP003708.
XX
PR 31-MAR-2000; 2000DE-01016013.
XX
PA (IPFP-) IPF PHARM GMBH.
PA (FORS/) FORSSMANN U.
XX
PI Forssmann W, Adermann K, Heitland A, Spodsberg N;
XX
DR WPI; 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.
XX
PS Disclosure; Page 9; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention
XX
SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL	360
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL	360

RESULT 4

AAU07614

ID AAU07614 standard; protein; 360 AA.

XX

AC AAU07614;

XX

DT 04-DEC-2001 (first entry)

XX

DE Human wild-type CCR2-64V polypeptide.

XX

KW Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis;
 KW single nucleotide polymorphism; hypercholesterolaemia.

XX

OS Homo sapiens.

XX

PN WO200162796-A1.

XX

PD 30-AUG-2001.

XX

PF 22-FEB-2001; 2001WO-GB000755.

XX

PR 22-FEB-2000; 2000GB-00004183.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Valdes AM, Groot PHE, Spurr NK;

XX

DR WPI; 2001-550086/61.

DR

N-PSDB; AAS12140.

XX

PT Diagnosing atherosclerosis or susceptibility to atherosclerosis in a
 PT subject, by determining a single nucleotide polymorphism in specific
 PT codon of a polynucleotide encoding human CCR2 receptor in genome of the
 PT subject.

XX

PS Claim 1; Page 21; 28pp; English.

KW respiratory virus infection; respiratory syncytial virus infection;
KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
XX
OS Homo sapiens.
XX
PN WO2003014153-A2.
XX
PD 20-FEB-2003.
XX
PF 12-AUG-2002; 2002WO-CA001248.
XX
PR 10-AUG-2001; 2001US-0311088P.
XX
PA (TOPI-) TOPIGEN PHARM INC.
XX
PI Renzi P, Zemzoumi K;
XX
DR WPI; 2003-256541/25.
DR N-PSDB; ABZ68878.
XX
PT Modulating viral infection of a cell, for treating or preventing
PT respiratory virus infections, bronchitis, pneumonia or asthma, by
PT modulating a binding interaction between a cell chemokine-receptor and a
PT surface protein of the virus.
XX
PS Disclosure; Page 82-84; 120pp; English.
XX
CC The present sequence represents human chemokine receptor CCR2. The
CC specification describes a method for modulating viral infection of a
CC cell. the method comprises modulating a binding interaction between a
CC cell chemokine-receptor and a surface protein of the virus. The proviso
CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
CC not HIV. The method is useful for treating or preventing respiratory
CC virus infection in vertebrates, more particularly respiratory syncytial
CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
CC bronchitis, pneumonia or asthma
XX
SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
          |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          |||

```

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 |||||

Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
 |||||

Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

RESULT 6

ABP81987

ID ABP81987 standard; protein; 360 AA.

XX

AC ABP81987;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human C-C chemokine receptor 2 protein SEQ ID NO:460.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW ulcer.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR N-PSDB; ABZ42835.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors

PT (GPCR), useful for diagnosing and designing drugs for treating conditions

PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or

PT autoimmune diseases.

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX

SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 6; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIIFTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIIFTIMIVYFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEVSA	360
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEVSA	360

RESULT 7

ADM67225

ID ADM67225 standard; protein; 360 AA.

XX

AC ADM67225;

XX

DT 03-JUN-2004 (first entry)

XX

DE Human adipocyte specific chemokine (C-C) receptor 2 protein SeqID 579.

XX

KW human; adipocyte specific; adipose tissue; anti-obesity;

KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;

KW adipogenesis; hypertension; cardiovascular disease; anorectic;

KW antidiabetic; hypotensive; chemokine (C-C) receptor 2.

XX

OS Homo sapiens.

XX

PN WO2004011618-A2.

XX

PD 05-FEB-2004.

XX

PF 29-JUL-2003; 2003WO-US023684.

XX

PR 29-JUL-2002; 2002US-0398785P.

PR 12-JUN-2003; 2003US-0478206P.

XX

PA (HMGE-) HMGNE INC.

XX

PI Chada K, Chouinard R, Ashar H, Sayed AMD;

XX

DR WPI; 2004-143846/14.

DR N-PSDB; ADM66946.

XX

PT Identifying adipocyte specific genes, useful for treating obesity or

PT diabetes, and for identifying drug targets, by differential gene

PT expression analysis between adipose tissue or stromal vascular tissue of

PT mice of different genotypes.

XX

PS Disclosure; SEQ ID NO 579; 91pp; English.

XX

CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polypeptide sequence is a human homologue of

XX
PA (GETH) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-329389/30.
DR N-PSDB; ADL82830.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
PS Claim 10; Fig 33; 695pp; English.
XX
CC The present invention relates to PRO proteins and their coding sequences.
CC The PRO proteins are useful for diagnosing and treating a B cell related
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
CC antigen unresponsiveness, selective IgA deficiency, selective IgM
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
CC medicament for treating a condition that is responsive to the PRO
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
CC coding sequences are useful as hybridization probes in chromosome and
CC gene mapping, in preparing PRO proteins, or in generating transgenic
CC animals or knockout animals, which in turn are useful in the development
CC and screening of therapeutically useful reagents.
XX
SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.8e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300

QY 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGGEQVSAGL 360
 |||
 Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGGEQVSAGL 360

RESULT 9
 AAU07613

ID AAU07613 standard; protein; 360 AA.

XX

AC AAU07613;

XX

DT 04-DEC-2001 (first entry)

XX

DE Human CCR2-64I polymorphic variant polypeptide.

XX

KW Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis;
 KW single nucleotide polymorphism; hypercholesterolaemia.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 64

FT /note= "Wild-type Val is replaced by Ile"

XX

PN WO200162796-A1.

XX

PD 30-AUG-2001.

XX

PF 22-FEB-2001; 2001WO-GB000755.

XX

PR 22-FEB-2000; 2000GB-00004183.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Valdes AM, Groot PHE, Spurr NK;

XX

DR WPI; 2001-550086/61.

DR N-PSDB; AAS12139.

XX

PT Diagnosing atherosclerosis or susceptibility to atherosclerosis in a
 PT subject, by determining a single nucleotide polymorphism in specific
 PT codon of a polynucleotide encoding human CCR2 receptor in genome of the
 PT subject.

XX

PS Claim 1; Page 20; 28pp; English.

XX

CC The invention relates to diagnosing atherosclerosis (or susceptibility
 CC to) in a subject by determining expression or activity of the human CCR2-
 CC 64I polypeptide (a polymorphic variant form of the human CCR2 receptor)
 CC or the CCR2-64V polypeptide (human CCR2 receptor), by screening for a
 CC single nucleotide polymorphism in codon 64 of the polynucleotide encoding
 CC the CCR2 receptor. This results in production of CCR2-64I, whereby
 CC polymorphic variants are associated with a lower incidence of
 CC atherosclerosis. The presence or amount of CCR2-64I/V in a sample can
 CC also be analysed. The sequences of the invention can be used for
 CC predicting the response of a patient to drug treatment, for predicting

CC the disease outcome in a patient and also for the production of a
CC treatment for hypercholesterolaemia. The sequence represents the
CC polymorphic variant polypeptide CCR2-64I
XX
SQ Sequence 360 AA;

Query Match 99.9%; Score 1899; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 2.3e-206;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
          |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
          |||:|||||
Db     61 MLVILILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          |||
Db    181 CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          |||
Db    241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
          |||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
```

RESULT 10

ABB56340

ID ABB56340 standard; protein; 360 AA.

XX

AC ABB56340;

XX

DT 18-FEB-2002 (first entry)

XX

DE Non-endogenous human GPCR protein, SEQ ID NO: 473.

XX

KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200177172-A2.

XX

PD 18-OCT-2001.

XX

PF 05-APR-2001; 2001WO-US011098.

XX

XX
 AC ADF56627;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Partial human monocyte chemoattractant protein 1 receptor.
 XX
 KW antiasthmatic; cardiant; hypotensive; antiallergic; neuroprotective;
 KW osteopathic; vulnerary; gene therapy; asthma; acute heart failure;
 KW hypertension; osteoporosis; allergy; dementia; ulcer; human;
 KW G protein coupled receptor; HGBER32;
 KW monocyte chemoattractant protein 1 receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2003165901-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 21-JUN-2002; 2002US-00176078.
 XX
 PR 05-JUN-1995; 95US-00461244.
 PR 25-JUN-1998; 98US-00104792.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Soppet DR, Li Y, Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-898052/82.
 XX
 PT New polynucleotide, useful for preparing a composition for diagnosing or
 PT treating e.g. asthma, acute heart failure, hypertension, osteoporosis,
 PT allergies, dementia or ulcers.
 XX
 PS Disclosure; SEQ ID NO 3; 28pp; English.
 XX
 CC The invention describes an isolated polynucleotide comprising a sequence
 CC encoding the polypeptide comprising a 355 residue amino acid sequence,
 CC given in the specification, a sequence encoding the polypeptide expressed
 CC by the DNA contained in ATCC Deposit No. 97187, a sequence that
 CC hybridises with, or that is at least 70 % identical to them, or a
 CC sequence fragment of them. The polynucleotide is useful for preparing a
 CC composition for diagnosing or treating asthma, acute heart failure,
 CC hypertension, osteoporosis, allergies, dementia or ulcers. This is the
 CC amino acid sequence of human monocyte chemoattractant protein 1 receptor
 CC starting at residue 40 and used in a comparison with human G protein
 CC coupled receptor HGBER32.
 XX
 SQ Sequence 347 AA;

Query Match 96.7%; Score 1838; DB 7; Length 347;
 Best Local Similarity 100.0%; Pred. No. 1.8e-199;
 Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKL 73
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKL 60

QY 74 KCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIL 133
 |||||
 Db 61 KCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIL 120

QY 134 LTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPY 193
 |||||
 Db 121 LTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPY 180

QY 194 FPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYF 253
 |||||
 Db 181 FPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYF 240

QY 254 LFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 313
 |||||
 Db 241 LFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 300

QY 314 RYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQVSAGL 360
 |||||
 Db 301 RYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQVSAGL 347

RESULT 12

AAR79165

ID AAR79165 standard; protein; 374 AA.

XX

AC AAR79165;

XX

DT 25-MAR-2003 (revised)

DT 29-DEC-1995 (first entry)

XX

DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.

XX

KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.

XX

OS Homo sapiens.

XX

Key	Location/Qualifiers
FT Domain	1. .48
FT	/label= extracellular
FT Domain	49. .70
FT	/label= transmembrane
FT Domain	80. .700
FT	/label= transmembrane
FT Domain	115. .136
FT	/label= transmembrane
FT Domain	154. .178
FT	/label= transmembrane
FT Domain	204. .231
FT	/label= transmembrane
FT Domain	244. .268
FT	/label= transmembrane
FT Domain	295. .313
FT	/label= transmembrane
FT Region	314. .375
FT	/label= carboxyl tail
XX	

PN WO9519436-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 11-JAN-1995; 95WO-US000476.
 XX
 PR 13-JAN-1994; 94US-00182962.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Charo I, Coughlin S;
 XX
 DR WPI; 1995-263866/34.
 DR N-PSDB; AAQ96297.
 XX
 PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocytic infiltrates.
 XX
 PS Claim 2; Fig 1; 84pp; English.
 XX
 CC To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
 CC HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pFROG and probed with the PCR product. A 2.1
 CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC sequence first obtd. from the 5' UTR through the putative seventh
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxyl
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 2; Length 374;
 Best Local Similarity 95.5%; Pred. No. 3e-178;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 Qy 61 MLVVLILINCKKCLKLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 MLVVLILINCKKCLKLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180


```

      |||
Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Qy      181 CQKEDSVYVCGPYFPRGWNNEFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
      |||
Db      181 CQKEDSVYVCGPYFPRGWNNEFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
Qy      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
      |||
Db      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
Qy      301 NPIIYAFVGEKFRRLSVFFRKHITKRECKQCPV 334
      |||
Db      301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

```

RESULT 13

AAG80107

ID AAG80107 standard; protein; 374 AA.

XX

AC AAG80107;

XX

DT 17-JAN-2002 (first entry)

XX

DE Human CCR2a protein.

XX

KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.

XX

OS Homo sapiens.

XX

PN WO200172830-A2.

XX

PD 04-OCT-2001.

XX

PF 02-APR-2001; 2001WO-EP003708.

XX

PR 31-MAR-2000; 2000DE-01016013.

XX

PA (IPFP-) IPF PHARM GMBH.

PA (FORS/) FORSSMANN U.

XX

PI Forssmann W, Adermann K, Heitland A, Spodsberg N;

XX

DR WPI; 2001-626256/72.

XX

PT Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.

XX

PS Disclosure; Page 9; 26pp; German.

XX

CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in

CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

XX

SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 4; Length 374;
 Best Local Similarity 95.5%; Pred. No. 3e-178;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLEWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLEWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPV	334
		: :	
Db	301	NPIIYAFVGEKFR---SLF---HIALG-CRIAPL	327

RESULT 14.

ABU09083

ID ABU09083 standard; protein; 374 AA.

XX

AC ABU09083;

XX

DT 23-JUL-2003 (first entry)

XX

DE Human chemokine receptor-2 (CKR-2) polypeptide.

XX

KW Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor;

Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Qy 181 CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
 Qy 241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPV 334
 |||||||||||| | : | || | : | :
 Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 15

ADD44861

ID ADD44861 standard; protein; 374 AA.

XX

AC ADD44861;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P41597, SEQ ID NO 10292.

XX

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; P41597.

XX

PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 374 AA;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAEVGEKFRRYLSVFFRKHITKRFCQCPV	334
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Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

Search completed: January 24, 2005, 21:43:12
Job time : 107.921 secs

OM protein - protein search, using sw model

Run on: January 24, 2005, 21:37:00 ; Search time 26.9755 Seconds
(without alignments)
885.044 Million cell updates/sec

Title: US-10-791-166-4
Perfect score: 1900
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVSTSTNPSTGQEVSAGL 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	
1	1900	100.0	360	1	US-08-450-393A-4	Sequence 4, Appli
2	1900	100.0	360	3	US-08-446-669-4	Sequence 4, Appli
3	1900	100.0	360	3	US-09-045-583-50	Sequence 50, Appl
4	1900	100.0	360	4	US-09-534-185-50	Sequence 50, Appl
5	1900	100.0	360	4	US-09-131-827A-2	Sequence 2, Appli
6	1900	100.0	360	4	US-09-625-573-4	Sequence 4, Appli
7	1900	100.0	360	5	PCT-US95-00476-4	Sequence 4, Appli
8	1899	99.9	360	4	US-09-131-827A-20	Sequence 20, Appl
9	1873	98.6	360	4	US-08-833-752-7	Sequence 7, Appli
10	1873	98.6	360	4	US-09-938-719-7	Sequence 7, Appli
11	1849	97.3	360	3	US-09-045-583-51	Sequence 51, Appl

12	1849	97.3	360	4	US-09-534-185-51	Sequence 51, Appl
13	1838	96.7	347	1	US-08-461-244-3	Sequence 3, Appli
14	1651.5	86.9	374	1	US-08-450-393A-2	Sequence 2, Appli
15	1651.5	86.9	374	3	US-08-446-669-2	Sequence 2, Appli
16	1651.5	86.9	374	4	US-10-039-659A-14	Sequence 14, Appl
17	1651.5	86.9	374	4	US-09-625-573-2	Sequence 2, Appli
18	1651.5	86.9	374	5	PCT-US95-00476-2	Sequence 2, Appli
19	1568.5	82.6	344	3	US-08-466-343D-9	Sequence 9, Appli
20	1568.5	82.6	344	4	US-09-502-784A-9	Sequence 9, Appli
21	1473	77.5	329	4	US-09-502-783A-9	Sequence 9, Appli
22	1473	77.5	329	4	US-09-339-912A-9	Sequence 9, Appli
23	1386	72.9	354	3	US-08-724-984A-2	Sequence 2, Appli
24	1371	72.2	352	3	US-09-517-605-5	Sequence 5, Appli
25	1370	72.1	352	3	US-09-045-583-52	Sequence 52, Appl
26	1370	72.1	352	4	US-09-534-185-52	Sequence 52, Appl
27	1364	71.8	352	3	US-09-087-232A-13	Sequence 13, Appl
28	1364	71.8	352	3	US-08-861-105-14	Sequence 14, Appl
29	1364	71.8	352	3	US-08-575-967A-2	Sequence 2, Appli
30	1364	71.8	352	4	US-08-833-752-5	Sequence 5, Appli
31	1364	71.8	352	4	US-09-796-202-1	Sequence 1, Appli
32	1364	71.8	352	4	US-09-938-719-5	Sequence 5, Appli
33	1364	71.8	352	4	US-08-771-276-2	Sequence 2, Appli
34	1364	71.8	352	4	US-08-771-276-20	Sequence 20, Appl
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36	1356	71.4	352	4	US-09-502-784A-2	Sequence 2, Appli
37	1356	71.4	352	4	US-09-339-912A-2	Sequence 2, Appli
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41	1036	54.5	355	3	US-08-446-669-5	Sequence 5, Appli
42	1036	54.5	355	3	US-09-239-938-1	Sequence 1, Appli
43	1036	54.5	355	4	US-09-886-319A-14	Sequence 14, Appl
44	1036	54.5	355	4	US-10-039-659A-13	Sequence 13, Appl
45	1036	54.5	355	4	US-09-961-068-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-450-393A-4

; Sequence 4, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-4

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Query Match          100.0%; Score 1900; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKCLKLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKCLKLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
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Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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Db    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

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RESULT 2

US-08-446-669-4

; Sequence 4, Application US/08446669

; Patent No. 6132987

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; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-4

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Query Match          100.0%; Score 1900; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        |||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

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 Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
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 Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

RESULT 3

US-09-045-583-50

; Sequence 50, Application US/09045583
 ; Patent No. 6287805
 ; GENERAL INFORMATION:
 ; APPLICANT: Graham, Gerard J. et al.
 ; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/045,583
 ; FILING DATE: 20-MAR-98
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MNI-044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 360 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal

US-09-045-583-50

Query Match 100.0%; Score 1900; DB 3; Length 360;
 Best Local Similarity 100.0%; Pred. No. 8.1e-151;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNEHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNEHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI	300
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RESULT 4

US-09-534-185-50

; Sequence 50, Application US/09534185

; Patent No. 6403767

; GENERAL INFORMATION:

; APPLICANT: Graham, Gerard J. et al.

; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/534,185

; FILING DATE: 24-Mar-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/045,583

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

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; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

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Query Match          100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 MLVVLILINCKKCLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
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Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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Db    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFERRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
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RESULT 5

US-09-131-827A-2

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; Sequence 2, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10

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; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
          |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          |||
Db    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCCKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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RESULT 6

US-09-625-573-4

; Sequence 4, Application US/09625573
; Patent No. 6730301

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-625-573-4

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Query Match          100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

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RESULT 7
 PCT-US95-00476-4
 ; Sequence 4, Application PC/TUS9500476
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; TITLE OF INVENTION: PROTEIN RECEPTORS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Robbins, Berliner & Carson
 ; STREET: 201 N. Figueroa Street, 5th Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90012-2628
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/00476
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Berliner, Robert
 ; REGISTRATION NUMBER: 20,121
 ; REFERENCE/DOCKET NUMBER: 5555-291
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-977-1001
 ; TELEFAX: 310-977-1003
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 360 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 PCT-US95-00476-4

Query Match 100.0%; Score 1900; DB 5; Length 360;
 Best Local Similarity 100.0%; Pred. No. 8.1e-151;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
 Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240


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Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
Qy      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Db      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy      301 NPIIYAFVGEKFRRLSVFFRKHITKRCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
Db      301 NPIIYAFVGEKFRRLSVFFRKHITKRCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

```

RESULT 8

US-09-131-827A-20

; Sequence 20, Application US/09131827A

; Patent No. 6600030

; GENERAL INFORMATION:

; APPLICANT: Dean, Michael

; APPLICANT: O'Brien, Stephen J.

; APPLICANT: Smith, Michael

; APPLICANT: Carrington, Mary

; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A

; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE

; FILE REFERENCE: 14014.0333

; CURRENT APPLICATION NUMBER: US/09/131,827A

; CURRENT FILING DATE: 1998-08-10

; PRIOR APPLICATION NUMBER: 60/055,659

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-131-827A-20

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Query Match          99.9%; Score 1899; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 9.8e-151;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db      61 MLVILILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy      121 HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
Db      121 HIGYFGGIIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy      241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

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Db      241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
Qy      301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
Db      301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

```

RESULT 9

US-08-833-752-7

; Sequence 7, Application US/08833752

; Patent No. 6448375

; GENERAL INFORMATION:

; APPLICANT: SAMSON, MICHEL

; APPLICANT: PARMENTIER, MARC

; APPLICANT: VASSART, GILBERT

; APPLICANT: LIBERT, FREDERICK

; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/833,752

; FILING DATE: 9-APR-1997

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E

; REGISTRATION NUMBER: 34,115

; REFERENCE/DOCKET NUMBER:

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6448375e

US-08-833-752-7

Query Match 98.6%; Score 1873; DB 4; Length 360;

Best Local Similarity 98.3%; Pred. No. 1.4e-148;

Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

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Qy 61 MLVVILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 |||||:|||||
 Db 61 MLVVILINCKKLKCLTDIYLLNLAISDLLFIITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 |||||:|||||
 Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
 |||||:|||||
 Db 181 CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 |||||:|||||
 Db 241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
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 Db 301 NPIIYAFVGEKFRRYISVFFRKHIXXXFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

RESULT 10

US-09-938-719-7

; Sequence 7, Application US/09938719

; Patent No. 6692938

; GENERAL INFORMATION:

; APPLICANT: SAMSON, MICHEL

; PARMENTIER, MARC

; VASSART, GILBERT

; LIBERT, FREDERICK

; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/938,719

; FILING DATE: 24-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/626,939

; FILING DATE: 27-JULY-2000

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E

; REGISTRATION NUMBER: 34,115

; REFERENCE/DOCKET NUMBER: <Unknown>

; INFORMATION FOR SEQ ID NO: 7:

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;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 360 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: No. 6692938e
;      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-938-719-7

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Query Match          98.6%; Score 1873; DB 4; Length 360;
Best Local Similarity 98.3%; Pred. No. 1.4e-148;
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGN 60
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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGN 60

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        |||
Db      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFIITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db      181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy      241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTTHCCI 300
        |||
Db      241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQAIQVTETLGMTTHCCI 300

Qy      301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
        |||
Db      301 NPIIYAFVGEKFRRYISVFFRKHIXXXFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

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RESULT 11

US-09-045-583-51

; Sequence 51, Application US/09045583

; Patent No. 6287805

; GENERAL INFORMATION:

; APPLICANT: Graham, Gerard J. et al.

; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

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;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/045,583
;   FILING DATE: 20-MAR-98
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Mandragouras, Amy E.
;   REGISTRATION NUMBER: 36,207
;   REFERENCE/DOCKET NUMBER: MNI-044
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617)227-7400
;   TELEFAX: (617)742-4214
;   INFORMATION FOR SEQ ID NO: 51:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 360 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
US-09-045-583-51

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Query Match          97.3%; Score 1849; DB 3; Length 360;
Best Local Similarity 97.2%; Pred. No. 1.4e-146;
Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKSLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVEASVPGIIFTK 180
        |||
Db    121 HIGYLGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVEASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRLIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTRQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
        |||
Db    301 NPIIYAFVGEKFRRYLSMFFRKYITKRFECKQCPVFYRETVDGVTSTNTPSTAEQEVSAAGL 360

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RESULT 12

US-09-534-185-51

; Sequence 51, Application US/09534185

; Patent No. 6403767

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; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767e1 Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

```

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Query Match          97.3%; Score 1849; DB 4; Length 360;
Best Local Similarity 97.2%; Pred. No. 1.4e-146;
Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||||||
Db      1 MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLLILINCKKCLKLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        |||||||
Db     61 MLVVLLILINCKKLSLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYLGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

```

Qy 181 CQKEDSVYVCGPYFPRGWNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
 ||:||||:||||||||||||||||||||||||||||||||||||||
 Db 181 CQEEDSVYICGPYFPRGWNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
 Qy 241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 |||:||||||||||||||||||||||||||||||||||||||
 Db 241 AVRLIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTRQLDQATQVTETLGMTHCCI 300
 Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
 ||||||||||||||||:||||:||||||||||||||||||||||
 Db 301 NPIIYAFVGEKFRRYLSMFFRKYITKRECKQCPVFYRETVDGVTSTNTPSTAEQEVSAAGL 360

RESULT 13

US-08-461-244-3

; Sequence 3, Application US/08461244

; Patent No. 5776729

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.

; APPLICANT: Yi, Li

; APPLICANT: Ruben, Steven M.

; APPLICANT: Rosen, Craig A.

; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

; ADDRESSEE: STUART & OLSTEIN

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,244

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Ferraro, Gregory D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-445

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 347 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-461-244-3

Query Match 96.7%; Score 1838; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      14 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKL 73
      |||
Db      1 NESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKL 60

Qy      74 KCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIIL 133
      |||
Db      61 KCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIIL 120

Qy     134 LTIDRYLAIVHAVFALKARTVTFGVTVSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPY 193
      |||
Db     121 LTIDRYLAIVHAVFALKARTVTFGVTVSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPY 180

Qy     194 FPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYF 253
      |||
Db     181 FPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYF 240

Qy     254 LEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 313
      |||
Db     241 LEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 300

Qy     314 RYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
      |||
Db     301 RYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 347
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RESULT 14

US-08-450-393A-2

; Sequence 2, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,393A

; FILING DATE: May 25, 1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:


```

; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2

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Query Match          86.9%; Score 1651.5; DB 1; Length 374;
Best Local Similarity 95.5%; Pred. No. 4.4e-130;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNEFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNEFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRYYLSVFFRKHITKRECKQCPV 334
        |||
Db    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

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RESULT 15

US-08-446-669-2

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; Sequence 2, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square

```

```

; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-2

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Query Match      86.9%; Score 1651.5; DB 3; Length 374;
Best Local Similarity 95.5%; Pred. No. 4.4e-130;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNEFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNEFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRLSVFFRKHITKRECKQCPV 334
        |||
Db    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

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Search completed: January 24, 2005, 21:49:30
Job time : 27.9755 secs

OM protein - protein search, using sw model

Run on: January 24, 2005, 21:36:30 ; Search time 24.5232 Seconds
(without alignments)
1412.462 Million cell updates/sec

Title: US-10-791-166-4
Perfect score: 1900
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVSTSTNTPSTGEQEVSAAGL 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1900	100.0	360	2	JC2443	chemokine (C-C) re
2	1651.5	86.9	374	2	I38450	chemokine (C-C) re
3	1364	71.8	352	2	A43113	chemokine (C-C) re
4	1036	54.5	355	2	A45177	chemokine (C-C) re
5	1010.5	53.2	359	2	I49341	MIP-1 alpha recept
6	963.5	50.7	355	2	I49339	macrophage inflamm
7	951	50.1	355	2	G02436	chemokine (C-C) re
8	871	45.8	360	2	JC4587	chemokine (C-C) re
9	862.5	45.4	360	2	A57160	chemokine (C-C) re
10	822.5	43.3	383	2	S55594	G protein-coupled
11	778.5	41.0	356	2	I49340	MIP-1 alpha recept
12	751	39.5	355	2	JC5067	G protein-coupled
13	722.5	38.0	354	2	I58186	probable G protein

14	708	37.3	355	2	JC4304	orphan G protein-c
15	649.5	34.2	344	2	JC5942	chemokine receptor
16	581.5	30.6	378	2	B55735	lymphocyte-specifi
17	569	29.9	378	2	A55735	G protein-coupled
18	567.5	29.9	378	2	A45680	G protein-coupled
19	563	29.6	369	2	JC5068	G protein-coupled
20	547	28.8	360	2	A53611	interleukin-8 rece
21	540.5	28.4	355	2	JQ1231	interleukin-8 rece
22	540.5	28.4	359	2	A48921	interleukin-8 rece
23	536.5	28.2	358	2	A53752	interleukin-8 rece
24	532.5	28.0	356	2	S42096	interleukin-8 rece
25	532	28.0	367	2	JE0349	interferon-inducib
26	528.5	27.8	333	2	I65989	G protein-coupled
27	528.5	27.8	350	2	A39445	interleukin-8 rece
28	515.5	27.1	352	2	G00048	fusin (LESTRA) - c
29	515	27.1	353	2	S28787	neuropeptide Y/pep
30	512.5	27.0	352	2	A45747	neuropeptide Y/pep
31	495.5	26.1	350	2	JN0621	G protein-coupled
32	486.5	25.6	359	2	S15403	angiotensin II rec
33	480.5	25.3	359	2	A42656	angiotensin II rec
34	480	25.3	374	2	S42628	G protein-coupled
35	475.5	25.0	359	2	JC2134	angiotensin II rec
36	474.5	25.0	359	2	JC1104	angiotensin II rec
37	474.5	25.0	359	2	S44425	angiotensin II rec
38	472.5	24.9	359	2	JH0621	angiotensin II rec
39	471.5	24.8	359	2	JQ1516	angiotensin II rec
40	469.5	24.7	359	2	JC1194	angiotensin II rec
41	468.5	24.7	359	2	I51372	angiotensin II rec
42	466	24.5	359	2	A48857	angiotensin II rec
43	465.5	24.5	374	2	S32785	G protein-coupled
44	465	24.5	327	2	S56162	MDCR15 protein - h
45	465	24.5	372	2	S26667	G protein-coupled

ALIGNMENTS

RESULT 1

JC2443

chemokine (C-C) receptor 2, splice form B - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor;

monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C;Accession: JC2443; I38463

R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.

Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994

A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor.

A;Reference number: JC2443; MUID:94324942; PMID:8048929

A;Accession: JC2443

A;Molecule type: mRNA

A;Residues: 1-360 <YAM>

A;Cross-references: UNIPROT:P41597; DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247

R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

A;Reference number: A53477; MUID:94195821; PMID:8146186

A;Accession: I38463

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-360 <RES>

A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558

C;Genetics:

A;Gene: GDB:CMKBR2

A;Cross-references: GDB:337364; OMIM:601267

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F;43-70/Domain: transmembrane #status predicted <TM1>

F;81-100/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;154-178/Domain: transmembrane #status predicted <TM4>

F;207-226/Domain: transmembrane #status predicted <TM5>

F;244-268/Domain: transmembrane #status predicted <TM6>

F;287-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1900; DB 2; Length 360;

Best Local Similarity 100.0%; Pred. No. 1.6e-156;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120
          |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVVFNGAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
          |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNEHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240
          |||
Db    181 CQKEDSVYVCGPYFPRGWNNEHTIMRNILGLVLPLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
          |||
Db    241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
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RESULT 2

I38450

chemokine (C-C) receptor 2, splice form A - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor;

monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004

C;Accession: I38450

R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

A;Reference number: A53477; MUID:94195821; PMID:8146186

A;Accession: I38450

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <RES>

A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556

C;Genetics:

A;Gene: GDB:CMKBR2

A;Cross-references: GDB:337364; OMIM:601267

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F;44-68/Domain: transmembrane #status predicted <TM1>

F;79-99/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;154-178/Domain: transmembrane #status predicted <TM4>

F;208-226/Domain: transmembrane #status predicted <TM5>

F;244-265/Domain: transmembrane #status predicted <TM6>

F;292-309/Domain: transmembrane #status predicted <TM7>

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;32-277,113-190/Disulfide bonds: #status predicted

Query Match 86.9%; Score 1651.5; DB 2; Length 374;

Best Local Similarity 95.5%; Pred. No. 4.8e-135;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|||||

Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
|||||

Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|||||

Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
|||||

Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

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Qy      241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETGLMTHCCI 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETGLMTHCCI 300

Qy      301 NPIIYAFVGEKFRRLSVFFRKHITKRFCCKQCPV 334
      ||||||||||||  |:|  ||  |:  |:
Db      301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

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Qy	142	IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----	RG	197
Db	130	VVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQKEGLHYTCSSHFYPYSQYQF		189
Qy	198	WNNFHTIMRNLGLVLP LLIMVICYSGILKTL LRCRNEKKRHRAVRVIFTIMIVYFLFWT		257
Db	190	WKNFQTLKIVILGLVLP LLVMVICYSGILKTL LRCRNEKKRHRAVRLIFTIMIVYFLFWA		249
Qy	258	PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLS		317
Db	250	PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL		309
Qy	318	VFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL		360
Db	310	VFFOKHIAKRECKCCSIFOOEAPERASSVYTRSTGEOEISVGL		352

A45177

N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004

R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.

A;Accession: A45177

A;Molecule type: mRNA

A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PIDN:AAA36543.1;
PID:g292417

A;Note: sequence extracted from NCBI backbone (NCBIP:124876)

J. Exp. Med. 177, 1421-1427, 1993

A;Reference number: I55671; MUID:93240122; PMID:7683036

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-355 <RES>

C;Genetics:

A;Cross-references: GDB:138446; OMIM:601159

C;Superfamily: vertebrate rhodopsin

F;36-60/Domain: transmembrane #status predicted <TM1>

F;108-129/Domain: transmembrane #status predicted <TM3>

F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-264/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;24-273,106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 54.5%; Score 1036; DB 2; Length 355;
 Best Local Similarity 56.4%; Pred. No. 6.4e-82;
 Matches 199; Conservative 56; Mismatches 90; Indels 8; Gaps 5;

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Qy      12 NTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCK 71
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Db      5 NTTED-YDTTTEFDYGDATPCQKVNERAFAQAQLLPPLYSLVFVIGLVGNILVVLVLVQYK 63

Qy      72 KKKCLTDIYLLNLAI S DLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIF 130
      : || : | || || || || || || || || | : : || || : || || : | | : || |
Db      64 RLKNMTSIYLLNLAI S DLLFLFTLPFWIDYK LKDDWVFGDAMCKILSGFYTGLYSEIFF 123

Qy      131 IILLTIDRYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTKCQKEDSVYVC 190
      || || || || || || || || || || || || || || || || || || || || || ||
Db      124 IILLTIDRYLAIVHAVFALRARTVTFGVITSIIWALAILASMPGLYFSKTQWEFTHHTC 183

Qy      191 GPYFP----RGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIF 246
      : || | | | : | : || || || || || || || || || || || || || || || ||
Db      184 SLHFPHESLREWKL FQALKLNLFGVLPLLVMIICYTGIIKILLRRPNEKK-SKAVRLIF 242

Qy      247 TIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCINPIIYA 306
      || | : || || || || || || || || || || || || || || || || || || || ||
Db      243 VIMIIFFLFWTPYNLTILISVFQDFLETHECEQSRHLDLAVQVTEVIAYTHCCVNPVIYA 302

Qy      307 FVGEKFRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEVSAG 359
      || || || || || || || || || || || || || || || || || || || || || ||
Db      303 FVGERFRKYLRQLFHRRAVAVHLVKWLPFLSVDRLERVSSST-SPSTGEHEL SAG 354
  
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RESULT 5

I49341

MIP-1 alpha receptor like-2 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49341

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49341

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-359 <RES>

A;Cross-references: UNIPROT:Q8K3M7; EMBL:U28406; NID:g881551; PID:g881552

C;Superfamily: vertebrate rhodopsin

```

Query Match          53.2%; Score 1010.5; DB 2; Length 359;
Best Local Similarity 53.5%; Pred. No. 1e-79;
Matches 193; Conservative 62; Mismatches 81; Indels 25; Gaps 6;

Qy      10  IRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILIN 69
      |:  || |  || ::||:  || |  :||::|: ||||| |||| | :|||:|||||
Db      8  IKTVVESFE--TTPYEYEWAPPCEKVRikelGswLLPPLYSLVFIIGLLGNMMVVLILIK 65

Qy      70  CKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAA-NEWVFGNAMCKLFTGLYHIGYFGGI 128
      :||: :||:| | ||||| ||| :| | |  ||| ||: |||: :| |: :  |
Db      66  YRKLQIMTNIYLFNLAISDLLFLFTVPFWIHYVLWNEWGFGHYMCKMLSGFYLYALYSEI 125

Qy      129 FFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVY 188
      ||||| ||||| ||||| :||| |  :||:| | :| |:| || :|  :
Db      126 FFIILLTIDRYLAIVHAVFALRARTVTFATITSITWGLAGLALPEFIFHESQDSFGEF 185

Qy      189 VCGPYFPRG----WNNFHTIMRNILGLVLPLLIMVICYSGILKTLRLCRNEKKRHRAVRV 244
      | | :| |  |  || :  || | ||||:||||| |:||| | ||:|:|:|
Db      186 SCSPRYPEGEEDSWKRFHALRMNIFGLALPLLVMVICYSGIIKTLRLCPN-KKKHKAIRL 244

Qy      245 IFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPII 304
      || :|||:|:|||||:|:| :|  |  ::|| :  || | |||| :  ||||:|:|
Db      245 IFVVMIVFFIFWTPYNLVLLFSAFHSTFLETSCEQSKHLDLAMQVTEVIAYTHCCVNPVI 304

Qy      305 YAFVGEKFRRYLSVFFRKHITKRfCKQCPVFYRETV-----DGVtSTNTPStGEQEV 356
      |||||:|:|:| :|| ::  |  | :  :| ||: :|||||:
Db      305 YAFVGERFRKHLRLFFHRNVQ-----FTWENIFQFLPGEENGRTSSVSPStGEQEI 355

Qy      357 S 357
      |
Db      356 S 356

```

Query Match 50.7%; Score 963.5; DB 2; Length 355;
Best Local Similarity 52.3%; Pred. No. 1.2e-75;
Matches 181; Conservative 65; Mismatches 89; Indels 11; Gaps 5;

Qy 21 TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGVGNMLVVLILINCKKLKCLTDIY 80
 || ||| || | : || ||||| ||| :||:|:|: :||: ||
 Db 13 TTEFDYGDSTPCQKTAVRAFGAGLLPPLYSIVFIIGVVGNVLVILVLMQHRRLQSMSTSIY 72

Qy 81 LLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLETGLYHIGYFGGIFFIILLTIDRY 139
 | |||:|:|:| || | : :||:|:| ||| :| |:| : ||||| ||||
 Db 73 LFNLAVSDLVFLFTLPFWIDYKLKDDWIFGDAMCKLLSGFYLLGLYSEIFFIILLTIDRY 132

Qy 140 LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---- 195
 ||||| |||:| |||| |::|:| || :| |:| : | | | : | |:|
 Db 133 LAIVHAVFALRARTVTLGIITSIITWALAILASMPALYFFKAQWEFTHRTCSPHFPYKSL 192

Qy 196 RGWNNEFTIMRNILGLVLPPLIMVICYSGILKTLRLCRNEKKRHRRAVRVIFTIMIVYFLE 255
 : | | : |:|:| |||:|:|:|:| || | :|: :|:| || |::| |
 Db 193 KQWKRFQALKLNLLGLLPLLVMIICYAGIIRILLR-RPSEKKVKAVRLIFAITLLFFLL 251

Qy 256 WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRY 315
 ||||: : :|: : || : || | ||| : |||:| ||| |||:| :|
 Db 252 WTPYNLSVFVSAFQDVLFNQCQSKHLDLQVTEVIAYTHCCVNPIIYVFGGERFWKY 311

Qy 316 LSVFFRKHITKRECKQCPVFYRETVDGV--TSTNTPSTGEQEVSA 359
 | |:|: | | :|| : ||: |||| |:| |
 Db 312 LRQLFQRHVAIPLAKWLPFL---SVDQLERTSSISPSTGEHEL 354

RESULT 7

G02436

chemokine (C-C) receptor 3 - human

N;Alternate names: C-C CKR-3

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C;Accession: G02436; A57237

R;Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A;Reference number: H01272

A;Accession: G02436

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-355 <PON>

A;Cross-references: UNIPROT:P51677; EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561

R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.

A;Reference number: A57237; MUID:95348056; PMID:7622448

A;Accession: A57237

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>

A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580

A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1, differs from the published sequence in having 281-Leu

C;Genetics:

A;Gene: GDB:CMKBR3

A;Cross-references: GDB:579624; OMIM:601268

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein;
 transmembrane protein
 F;36-60/Domain: transmembrane #status predicted <TM1>
 F;71-91/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-261/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;24-273,106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
 predicted

Query Match 50.1%; Score 951; DB 2; Length 355;
 Best Local Similarity 52.6%; Pred. No. 1.4e-74;
 Matches 180; Conservative 65; Mismatches 89; Indels 8; Gaps 5;

Qy	21	TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY	80
		:: : : : : :: : : :	
Db	14	TSYYD-DVGLLCEKADTRALMAQFVPPLYSLVFTVGLLGNVVVMILIKYRRRLRIMTNIY	72
Qy	81	LLNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLETGLYHIGYFGGIFFIILLTIDRY	139
		: : : : :	
Db	73	LLNLAISDLLFLVTLFPWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRY	132
Qy	140	LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR---	196
		: : : : : : : :	
Db	133	LAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYPEDTV	192
Qy	197	-GWNNEFTIMRNILGLVLPPLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIVYFLF	255
		: : : : : :: :	
Db	193	YSWRHFHTLRMTIFCLVLPPLVMAICYTGIKTLRLCPS-KKKYKAIRLIFVIMAVFFIF	251
Qy	256	WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRY	315
		: :: : : : : :	
Db	252	WTPYNVAILLSSYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMPVIYAFVGERFRKY	311
Qy	316	LSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV	357
		: : : : :	
Db	312	LRHFFHRHLLMHLGRYIPFLPSEKLER-TSSVSPSTAEP	352

RESULT 8

JC4587

chemokine (C-C) receptor 4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: JC4587

R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of
 chemokines to murine and human CC CKR-4.

A;Reference number: JC4587; MUID:96136324; PMID:8573157

A;Accession: JC4587

A;Molecule type: mRNA

A;Residues: 1-360 <HOO>

A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1;
PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II)
#status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
predicted

RESULT 9

RESULT 10

S55594

G protein-coupled receptor E1 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C;Accession: S55594

R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A;Title: The DNA sequence of equine herpesvirus 2.

A;Reference number: S55594; MUID:95302501; PMID:7783207

A;Accession: S55594

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-383 <TEL>

A;Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:AAC13788.1;

PID:g695173

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 43.3%; Score 822.5; DB 2; Length 383;
Best Local Similarity 47.9%; Pred. No. 1.9e-63;
Matches 162; Conservative 60; Mismatches 107; Indels 9; Gaps 4;

```

Qy      4 TSRSRFFIRNTNESGEEVTTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNM 61
      | : : : : | | : | | | | : | | : : | | | | : | : | :
Db      32 TTIASLVPSTNSSDYDDLDDVDYEEAPCYKSDTTRLAAQVVPALYLLVFLFGLLGNI 91

Qy      62 LVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAH--SAANEWVFGNAMCKLFTGL 119
      | | : | : | | : | | : : | | | | | | : | | | : | : | :
Db      92 LVVIIVIRYMKIKNLTNMLLLNLAISDLLFLLTLFPFWMHYIGMYHDWTFGISLCKLLRGV 151

Qy      120 YHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFT 179
      : : : : | | | | : | | | : | : | | : | | | : | : |
Db      152 CYMSLYSQVFCIILLTVDRYLAVVYAVTALRFRTVTCGIVTCVCTWFLAGLLSLPEFFFH 211

Qy      180 KCQKEDSVYVCGPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNE 235
      | : : | | : | | | : | : | : | | | : | : | : |
Db      212 GHQDDNGRVQCDPYPEMSTNVWRRHAVAKVIMLSLILPLLIMAVCYVVIIRLLR-RPS 270

Qy      236 KKRHRAVRVIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGM 295
      | | : : | : | | | : | | : | | | | | : | : | : | : | :
Db      271 KKKYKAIRLIFVIMVAYFVFWTPYNIIVLLLSFTHATLLNLQCALSSNLDMALLITKT VAY 330

Qy      296 THCCINPIIYAFVGEKFRRYLSVFFRKHITKRECKQCP 333
      | | | | : | | | | | | : | | : : | | |
Db      331 THCCINPVIYAFVGEKFRRHLYHFFHTYVAIYLCKYIP 368

```

RESULT 11

I49340

MIP-1 alpha receptor like-1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I49340

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.

A;Reference number: I49339; MUID:95340546; PMID:7542241

A;Accession: I49340

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-356 <RES>

A;Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550

C;Superfamily: vertebrate rhodopsin

Query Match 41.0%; Score 778.5; DB 2; Length 356;
Best Local Similarity 45.2%; Pred. No. 1.1e-59;
Matches 154; Conservative 62; Mismatches 118; Indels 7; Gaps 4;

```
Qy      25 DYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNL 84
      | : | | : | : | | | | | | | : | : | | | : | | | | |
Db      18 DFMSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLIQHKRLRNMTSIYLFNL 77

Qy      85 AISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIV 143
      | | | | : | | | | : : | : | | | | | : | | | | | | | |
Db      78 AISDLVFLSTLPFWVDYIMKGDWIFGNAMCKEVS GFYYLGLYS DMFFITLLTIDRYLAVV 137

Qy     144 HAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR----GWN 199
      | | | | : | | | | | : : | | | : | | : | | : | | :
Db     138 HVVFALRARTVTFGIISSIITWVLAALVSIPCLYVFKSQMEFTYHTCRAILPRKSLIRFL 197

Qy     200 NFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHRRAVRVIFTIMIVYFLEWTPY 259
      | : | | | : | | | | : | | : | | | | | : : | | | |
Db     198 RFQALTMNIGLILPLLAMIIICYTRIINV LHR-RPNKKKAKVMRLIFVITLLFFLLAPY 256

Qy     260 NIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVF 319
      : : : | : : : | : | : : | | | | | : | | : | | |
Db     257 YLAAFVSAFEDVLEFTPSCLSRQQVDLSLMITEALAYTHCCVNPVIYVFVGKRFKRYLWQL 316

Qy     320 FRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
      | : | : | | | | | | | | | | | |
Db     317 FRRHTAITLPQWLP-FLSEDRAQRASARLPSTVEIETSADL 356
```

RESULT 12

JC5067

G protein-coupled receptor CKR-L1 - human

N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004

C;Accession: JC5067; G02776; G02387

R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes.

A;Reference number: JC5067; MUID:97040707; PMID:8886020

A;Accession: JC5067

A;Molecule type: DNA

A;Residues: 1-355 <ZAB>

A;Cross-references: UNIPROT:P51685; EMBL:279782; NID:g1668735; PIDN:CAB02142.1;
 PID:g1668736
 R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.;
 Santoni, A.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: H01714
 A;Accession: G02776
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <NAP>
 A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
 R;Bonner, T.I.
 submitted to the EMBL Data Library, January 1996
 A;Reference number: H01154
 A;Accession: G02387
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <BON>
 A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
 C;Comment: This protein belongs to the family of beta chemokine receptors.
 C;Genetics:
 A;Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1
 A;Cross-references: GDB:6053733; OMIM:601834
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein
 F;36-63/Domain: transmembrane #status predicted <TM1>
 F;73-94/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;200-222/Domain: transmembrane #status predicted <TM5>
 F;239-260/Domain: transmembrane #status predicted <TM6>
 F;281-304/Domain: transmembrane #status predicted <TM7>

Query Match 39.5%; Score 751; DB 2; Length 355;
 Best Local Similarity 41.2%; Pred. No. 2.6e-57;
 Matches 143; Conservative 69; Mismatches 121; Indels 14; Gaps 5;

Qy	20	VTTFFDYDY----GAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGNMLVVLILINCKKLKC	75
		: :: : : : : :	
Db	9	VTTVTDYYPDIFSSPCDAELIQTKGKLLAVFYCLLFVFSLLGNSLVILVLVVCCKLRS	68
Qy	76	LTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLT	135
		: : : : : : : : : : : ::	
Db	69	ITDVYLLNLALSDLLFVFSFPFQTYLLDQWVFGTVMCKVVSFGFYIYGFYSSMFFITLMS	128
Qy	136	IDRYLAIVHAVFALKARTVTFGVVTSVITWLIVAVFASVPGIIFTKCQKEDSVYVCGPYFP	195
		: : : : : : : : ::	
Db	129	VDRYLAVVHAVYALKVRTIRMGTTLCLAVWLTAIMATIPLLVFYQVASEDGLVQCYSFYN	188
Qy	196	R---GWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVY	252
		: : : : : : :	
Db	189	QQTLLKWKIFTNFKMNLGLLPFTIFMFCYIKILHQLKRCQNHNKT-KAIRLVLIIVVIAS	247
Qy	253	FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF	312
		: : : : : : :	
Db	248	LLFWVPFNVVLFSLHSMHILDGCSISQQLTYATHVTEIISFTHCCVNPVIYAFVGEKF	307

```

QY      313 RRYLSVFFRKHITKRF---CKQCPVFYRETVDGVTSTNTPSTGEQEV 356
      ::|| | :| :: | :| | ||: : :| | : |
Db      308 KKHLSEIFOKSCSOIFNYLGROMP---RESCEKSSSCOOHSSRSSSV 351

```

RESULT 13

I58186

probable G protein-coupled receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text change 09-Jul-2004

C;Accession: I58186

R; Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.

A;Reference number: I58186; MUID:94323113; PMID:8047298

A;Accession: I58186

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-354 <RES>

A;Cross-references: UNIPROT:P35411; EMBL:U04808; NID:q2558635; PIDN:AAB87093.1;

PID: q439861

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 38.0%; Score 722.5; DB 2; Length 354;

Best Local Similarity 46.2%; Pred. No. 7.4e-55;

Matches 160; Conservative 46; Mismatches 121; Indels 19; Gaps 8;

Qy 24 FDYDYGA-PCHKFDVKQIGAQLLPYLSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLL 82

Db 13 FEYDDSAEACYLGDIVAFGTIFLSIFYSLVFTEGLVGNLLVVLALTNSRKSKSITDIYLL 72

Qy 83 NLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIIFFIILLTIDRYLAI 142
|||:||||: ||| | : | : ||| ||| : |||:||||| :||| |||

Db 73 NLALSDLLFVATLPFWTHYLISHEGLHNAMCKLTTAFFFIGFFGGIFFITVISIDRYLAI 132

Qy 143 VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIIFTKCQKEDSVYVCGPYFPRGWNNFH 202

Db 133 VLAANSMNNRTVOHGV TISLG V WAAAILVASPOFMETK-RKDNE---CLGDYPEVLOETW 188

Qy 203 TIMR----NILGLVLPLLLIMVICYSGILKTLRLRCRNEKKRRHRAVRVIFTIMIVYFLFWTP 258
 ::| | | | | | | | | | | | : : | | : | | | : : | : : : | | | |

Db 189 PVLNRNSEVNILGFVLPLLIMSFYFRIVRTLFSCKNRKKA-RAIRLILLVVVFFLEWTP 247

QY 259 YNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSV 318
 ||||| | | : : | | | : : ||| : |||||

Db 248 YNIVIFLETLKFYNFFPSCGMKRDLRWALSVTETVAFSHCCLNPFIYAFAGEKFERRYLRH 307

QY 319 FFRKHITKRFCCKQCPVF-----YRETVDGVTSTNTPSTGEQEVS 357

Db 308 LYNKCLAV-LCGR-PVHAGFSTESORSRODSILSSLTHYTSEGEGS 351

RESULT 14

JC4304

orphan G protein-coupled receptor - human
 N;Alternate names: V28 protein
 C;Species: Homo sapiens (man)
 C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
 C;Accession: JC4304
 R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
 Gene 163, 295-299, 1995
 A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely
 related to genes for chemokine receptors and is expressed in lymphoid and
 neural tissues.
 A;Reference number: JC4304; MUID:96011651; PMID:7590284
 A;Accession: JC4304
 A;Molecule type: mRNA
 A;Residues: 1-355 <RAP>
 A;Cross-references: UNIPROT:P49238; GB:U20350; NID:g665580; PIDN:AAA91783.1;
 PID:g665581
 A;Experimental source: peripheral blood mononuclear cell
 C;Comment: This protein is a cell-surface receptor which recognizes
 extracellular signals and transduces those signals into an intracellular
 response.
 C;Comment: This protein is a key regulator of many immune and homeostatic
 responses, and interacts between the nervous and immune systems.
 C;Genetics:
 A;Gene: v28
 A;Map position: 3pter-p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
 F;35-57/Domain: transmembrane #status predicted <TM1>
 F;66-88/Domain: transmembrane #status predicted <TM2>
 F;104-125/Domain: transmembrane #status predicted <TM3>
 F;146-165/Domain: transmembrane #status predicted <TM4>
 F;197-217/Domain: transmembrane #status predicted <TM5>
 F;230-254/Domain: transmembrane #status predicted <TM6>
 F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 37.3%; Score 708; DB 2; Length 355;
 Best Local Similarity 46.8%; Pred. No. 1.3e-53;
 Matches 145; Conservative 47; Mismatches 108; Indels 10; Gaps 5;

Qy	18	EEVTTFDY-DYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCL	76
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Db	6	ESVTENFEYDDLAEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSV	65
Qy	77	TDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFFIILLTI	136
		: : : : : :	
Db	66	TDIYLLNLALSDDLFEVATLPFWTHYLINEKGLHNAMCKFTTAAFFFIGFFGSIFFITVISI	125
Qy	137	DRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR	196
		: : : : : : : :	
Db	126	DRYLAIVLAANSNNRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKENE---CLGDYPE	181
Qy	197	GWNNFHTIMRNI----LGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVY	252
		: : : : : : : :	
Db	182	VLQEIWPVLRNVETNFLGFLPLLIMSYCYFRIIQTLSCKNHKKA-KAIKLILLVVIVF	240
Qy	253	FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF	312
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RESULT 15

JC5942

chemokine receptor - human

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence revision 16-Jul-1999 #text change 09-Jul-2004

C;Accession: JC5942

R; Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.

Biochem. Biophys. Res. Commun. 243, 264-268, 1998

A;Title: Cloning and characterization of a novel human chemokine receptor.

A;Reference number: JC5942; MUID:98139902; PMID:9473515

A;Accession: JC5942

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-344 <FAN>

A;Cross-references: UNIPROT:000421; GB:U97123; NID:q2897070; PIDN:AAC39595.1;

PID: α2897071

C;Superfamily: vertebrate rhodopsin

Query Match 34.2%; Score 649.5; DB 2; Length 344;

Best Local Similarity 43.0%; Pred. No. 1.4e-48;

Matches 128; Conservative 54; Mismatches 99; Indels 17; Gaps 5;

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Db	23	DEAEQC DKYDAQALSAQLVPSLCSAVFVIGVL D NLLVVLILVKYKGLKRVENIYLLNLAV	82
Qy	87	SDDLFLITLPLWAHSAANEWVF G NAMCKLFTGLYHI G YFGGIFFIILLTIDRYLAIVH-A	145
		: : : : : : : : :	
Db	83	SNLCFLLTL PFWAHAG-----GDPMCKILIGLYFVG L YSETFFNCLLT V QRYLVFLHKG	136
Qy	146	VEALKARTVT FGVVTSVITWLVA VFASVPGIIFTKCQKEDSVYVCG----PYFPRG---W	198
		: : : : :	
Db	137	NFFSARRRVPCGIITSVLAWVTAILATLPEYVVYKPQMEDQKYKCAFSRTPFLPADETFW	196
Qy	199	NNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVI FTIMIVYFLFWTP	258
		: : : : : : :	
Db	197	KHFLTLMKNISVLVLPLFI FTFLYVQMRKTL---RFREQRYSLFKLVFAIMVVFLLMWAP	253
Qy	259	YNIVILLNTFQE E FGLSNCESTS QLDQATQVTETLGMTHCCINPIIYA FVGEKFRRYL	316
		: : : : : : : : :	
Db	254	YNIAFFLSTFKEHFSLS D CKSSYNLDKSVHITKL I ATTHCCINPLLYA FL DGTFSKYL	311

Search completed: January 24, 2005, 21:48:28

Job time : 25.5232 secs

OM protein - protein search, using sw model

Run on: January 24, 2005, 21:47:41 ; Search time 97.6022 Seconds
(without alignments)
1332.595 Million cell updates/sec

Title: US-10-791-166-4
Perfect score: 1900
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVSTSTNPSTGEQEVSAAGL 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1900	100.0	360	9	US-09-131-827A-2	Sequence 2, Appli
2	1900	100.0	360	14	US-10-225-567A-460	Sequence 460, App
3	1900	100.0	360	14	US-10-164-649-50	Sequence 50, Appl
4	1900	100.0	360	14	US-10-239-423-64	Sequence 64, Appl
5	1900	100.0	360	14	US-10-439-845-8	Sequence 8, Appli
6	1900	100.0	360	16	US-10-741-601-285	Sequence 285, App
7	1900	100.0	360	16	US-10-741-601-286	Sequence 286, App
8	1900	100.0	360	17	US-10-791-592-4	Sequence 4, Appli
9	1900	100.0	360	17	US-10-791-166-4	Sequence 4, Appli
10	1900	100.0	360	17	US-10-700-313-8	Sequence 8, Appli
11	1899	99.9	360	9	US-09-131-827A-20	Sequence 20, Appl
12	1894	99.7	360	10	US-09-826-509-473	Sequence 473, App
13	1873	98.6	360	9	US-09-938-719-7	Sequence 7, Appli
14	1873	98.6	360	9	US-09-939-226-7	Sequence 7, Appli
15	1873	98.6	360	9	US-09-938-703-7	Sequence 7, Appli
16	1873	98.6	360	16	US-10-661-798-7	Sequence 7, Appli
17	1873	98.6	360	16	US-10-612-791-7	Sequence 7, Appli
18	1849	97.3	360	14	US-10-164-649-51	Sequence 51, Appl
19	1838	96.7	347	9	US-09-104-792-3	Sequence 3, Appli
20	1838	96.7	347	14	US-10-176-078-3	Sequence 3, Appli
21	1838	96.7	347	17	US-10-893-996-3	Sequence 3, Appli
22	1819.5	95.8	384	10	US-09-893-512-14	Sequence 14, Appl
23	1651.5	86.9	374	10	US-09-893-512-13	Sequence 13, Appl
24	1651.5	86.9	374	14	US-10-039-659-14	Sequence 14, Appl
25	1651.5	86.9	374	14	US-10-239-423-63	Sequence 63, Appl
26	1651.5	86.9	374	16	US-10-754-071-14	Sequence 14, Appl
27	1651.5	86.9	374	16	US-10-741-601-287	Sequence 287, App
28	1651.5	86.9	374	17	US-10-791-592-2	Sequence 2, Appli
29	1651.5	86.9	374	17	US-10-791-166-2	Sequence 2, Appli
30	1568.5	82.6	344	9	US-09-779-879A-9	Sequence 9, Appli
31	1568.5	82.6	344	9	US-09-779-880A-9	Sequence 9, Appli
32	1568.5	82.6	344	14	US-10-232-686-9	Sequence 9, Appli
33	1568.5	82.6	344	14	US-10-067-800-9	Sequence 9, Appli
34	1568.5	82.6	344	14	US-10-135-839-9	Sequence 9, Appli
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36	1473	77.5	329	9	US-09-195-662A-9	Sequence 9, Appli
37	1473	77.5	329	9	US-09-339-912A-9	Sequence 9, Appli
38	1473	77.5	329	9	US-09-502-783A-9	Sequence 9, Appli
39	1473	77.5	329	16	US-10-791-905-9	Sequence 9, Appli
40	1371	72.2	352	14	US-10-151-274-5	Sequence 5, Appli
41	1370	72.1	352	14	US-10-164-649-52	Sequence 52, Appl
42	1364	71.8	352	9	US-09-759-841-2	Sequence 2, Appli
43	1364	71.8	352	9	US-09-813-653-15	Sequence 15, Appl
44	1364	71.8	352	9	US-09-796-202-1	Sequence 1, Appli
45	1364	71.8	352	9	US-09-938-719-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-131-827A-2

; Sequence 2, Application US/09131827A

; Patent No. US20020038469A1


```
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2
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Best Local Similarity 100.0%; Pred. No. 7.2e-155;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNEHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
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Qy    241 AVRVIIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
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RESULT 2

US-10-225-567A-460

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; Sequence 460, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
```

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; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 460
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-460
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Query Match          100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.2e-155;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

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Qy    241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEVSA GL 360
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RESULT 3

US-10-164-649-50

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; Sequence 50, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-
Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
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; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
;
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-164-649-50

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Query Match          100.0%;  Score 1900;  DB 14;  Length 360;
Best Local Similarity 100.0%;  Pred. No. 7.2e-155;
Matches 360;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
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RESULT 5

US-10-439-845-8

; Sequence 8, Application US/10439845

; Publication No. US20030195348A1

; GENERAL INFORMATION:

; APPLICANT: Combadiere et al.,

; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS

; TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/439,845

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/864,458

; FILING DATE: May 28, 1997

; APPLICATION NUMBER: Provisional 60/018,508

; FILING DATE: May 28, 1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Haile, Lisa A.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 08830/030001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-10-439-845-8

Query Match 100.0%; Score 1900; DB 14; Length 360;

Best Local Similarity 100.0%; Pred. No. 7.2e-155;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNEFTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
Db	301	NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360

RESULT 6

US-10-741-601-285

; Sequence 285, Application US/10741601

; Publication No. US20040166519A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 285

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-741-601-285

Query Match 100.0%; Score 1900; DB 16; Length 360;
 Best Local Similarity 100.0%; Pred. No. 7.2e-155;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSIVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180

Db	121		HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181		CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181		CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241		AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	241		AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Qy	301		NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL	360
Db	301		NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL	360

RESULT 7

US-10-741-601-286

; Sequence 286, Application US/10741601

; Publication No. US20040166519A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 286

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-741-601-286

Query Match 100.0%; Score 1900; DB 16; Length 360;
 Best Local Similarity 100.0%; Pred. No. 7.2e-155;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Db	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK	180
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Db	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR	240
Qy	241	AVRVIFTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300

Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

QY 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
 |||

Db 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

RESULT 8

US-10-791-592-4

; Sequence 4, Application US/10791592

; Publication No. US20040219644A1

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

; PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/791,592

; FILING DATE: 01-Mar-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/625,573

; FILING DATE: 25-Jul-2000

; APPLICATION NUMBER: US/08/446,669

; FILING DATE: May 25, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard

; REGISTRATION NUMBER: 30,092

; REFERENCE/DOCKET NUMBER: UCAL-237/01US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-843-5000

; TELEFAX: 415-857-0663

; TELEX: 380816CooleyPA

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-791-592-4

Query Match 100.0%; Score 1900; DB 17; Length 360;
 Best Local Similarity 100.0%; Pred. No. 7.2e-155;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
        |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNEFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNEFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
        |||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
```

RESULT 9

US-10-791-166-4

; Sequence 4, Application US/10791166

; Publication No. US20040223968A1

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94306-2155

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/791,166

; FILING DATE: 01-Mar-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/625,573

; FILING DATE: 25-Jul-2000

; APPLICATION NUMBER: US/08/446,669

```

;          FILING DATE: May 25, 1995
;
;  ATTORNEY/AGENT INFORMATION:
;
;          NAME: Neeley, Richard
;          REGISTRATION NUMBER: 30,092
;          REFERENCE/DOCKET NUMBER: UCAL-237/01US
;
;  TELECOMMUNICATION INFORMATION:
;
;          TELEPHONE: 415-843-5000
;          TELEFAX: 415-857-0663
;          TELEX: 380816CooleyPA
;
;  INFORMATION FOR SEQ ID NO: 4:
;
;      SEQUENCE CHARACTERISTICS:
;
;          LENGTH: 360 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;
;      MOLECULE TYPE: protein
;
;      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-791-166-4

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```

Query Match          100.0%;  Score 1900;  DB 17;  Length 360;
Best Local Similarity 100.0%;  Pred. No. 7.2e-155;
Matches 360;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVI FTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AVRVI FTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTS QLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRYLSVFFRKHITKR FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 NPIIYAFVGEKFRRYLSVFFRKHITKR FCKQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360

```

RESULT 10

US-10-700-313-8

; Sequence 8, Application US/10700313

; Publication No. US20040259785A1

; GENERAL INFORMATION:

; APPLICANT: Combadiere et al.,

; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

```

; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/700,313
; FILING DATE: 31-Oct-2003
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,458
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-700-313-8

```

```

Query Match          100.0%;  Score 1900;  DB 17;  Length 360;
Best Local Similarity 100.0%;  Pred. No. 7.2e-155;
Matches 360;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|
Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|
Qy    121 HIGYFGGIFFIILLTDIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|
Db    121 HIGYFGGIFFIILLTDIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|
Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
|
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
|
Qy    241 AVRVIPTIMIVYFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|

```


RESULT 12

US-09-826-509-473

; Sequence 473, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated
Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

: PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEO ID NOS: 589

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; SOFTWARE: PatentIn Version 2.1
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; SEO ID NO 473

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-473

Query Match 99.7%; Score 1894; DB 10; Length 360;
Best Local Similarity 99.7%; Pred. No. 2.4e-154;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

[illegible]

Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKOIGAOLLPLYSLVFIFGEVGN 60

[illegible]

Db 61 MLVVLILINCKKCLKLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 | | | | | | | | | | | | | | | | | | | | | | | |

Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLP LLIMVICYSGILKTLRLCRNEKKRHR 240..

Db 181 COKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
| | | | | | | | | | | | | | | | | | | | | | | | |

Db 241 AKRVIFTIMIVYFLFWTPYNIVILLNTFOEFFGLSNCESTSOLDQATQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRLSVFFRKHITKRECKQCPVFFYRETVDGVTSTNTPSTGEQEVSAAGL 360

Db 301 NPIIYAFVGEKFBRYLSVFFRKHITKRECKOCPVFYRETVDGVTSTNTPSTGEOEVSAGL 360

RESULT 13
 US-09-938-719-7
 ; Sequence 7, Application US/09938719
 ; Patent No. US20020106742A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SAMSON, MICHEL
 ; PARMENTIER, MARC
 ; VASSART, GILBERT
 ; LIBERT, FREDERICK
 ; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
 ; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson & Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/938,719
 ; FILING DATE: 24-Aug-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/626,939
 ; FILING DATE: 27-JULY-2000
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Altman, Daniel E
 ; REGISTRATION NUMBER: 34,115
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 360 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. US20020106742A1e
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-938-719-7

Query Match 98.6%; Score 1873; DB 9; Length 360;
 Best Local Similarity 98.3%; Pred. No. 1.5e-152;
 Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	61	MLVVLILINCKKLKCLTDIYLLNLAISDLLFIITLPLWAHSAANEWVFGNAMCKLFTGLY	120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 |||||
 Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLMVICYSGILKTLLRCRNEKKRHR 240
 |||||
 Db 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLMVICYSGILKTLLRCRNEKKRHR 240
 Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 |||||
 Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQAIQVTETLGMTHCCI 300
 Qy 301 NPIIYAFVGEKFERRYLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360
 |||||:|||||
 Db 301 NPIIYAFVGEKFERRYISVFFRKHIXXFXCKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 14

US-09-939-226-7

; Sequence 7, Application US/09939226

; Patent No. US20020110805A1

; GENERAL INFORMATION:

; APPLICANT: SAMSON, MICHEL

; PARMENTIER, MARC

; VASSART, GILBERT

; LIBERT, FREDERICK

; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/939,226

; FILING DATE: 24-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/626,939

; FILING DATE: 2000-07-27

; ATTORNEY/AGENT INFORMATION:

; NAME: Altman, Daniel E

; REGISTRATION NUMBER: 34,115

; REFERENCE/DOCKET NUMBER: <Unknown>

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20020110805A1e
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-939-226-7

Query Match 98.6%; Score 1873; DB 9; Length 360;
Best Local Similarity 98.3%; Pred. No. 1.5e-152;
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
|
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
|
Db 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFIITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
|
Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNNEHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
|
Db 181 CQKEDSVYVCGPYFPRGWNNEHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
|
Db 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQAIQVTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
|
Db 301 NPIIYAFVGEKFRRYISVFFRKHIXXXFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360

RESULT 15

US-09-938-703-7

; Sequence 7, Application US/09938703

; Patent No. US20020110870A1

; GENERAL INFORMATION:

; APPLICANT: SAMSON, MICHEL

; PARMENTIER, MARC

; VASSART, GILBERT

; LIBERT, FREDERICK

; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 620 Newport Center Drive 16th Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: U.S.A.

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible


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;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/938,703
;      FILING DATE: 24-Aug-2001
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 09/626,939
;      FILING DATE: 2000-07-27
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Altman, Daniel E
;      REGISTRATION NUMBER: 34,115
;      REFERENCE/DOCKET NUMBER: <Unknown>
;      INFORMATION FOR SEQ ID NO: 7:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 360 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: No. US20020110870A1e
;      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-938-703-7

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Query Match          98.6%;  Score 1873;  DB 9;  Length 360;
Best Local Similarity 98.3%;  Pred. No. 1.5e-152;
Matches 354;  Conservative 2;  Mismatches 4;  Indels 0;  Gaps 0;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
        |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
        |||:|||||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFIITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
        |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
        |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
        |||
Db    241 AVRVIIFTIMIVYFLFWTPYNIIVILLNTFQEFFGLSNCESTSQLDQAIQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFERRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360
        |||:|||||
Db    301 NPIIYAFVGEKFERRYISVFFRKHIXXFKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360

```

```

Search completed: January 24, 2005, 22:04:52
Job time : 98.6022 secs

```

OM protein - protein search, using sw model

Run on: January 24, 2005, 21:28:29 ; Search time 125.559 Seconds
(without alignments)
1649.707 Million cell updates/sec

Title: US-10-791-166-4
Perfect score: 1900
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....DGVSTSTNPSTGQEVSAGL 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1845	97.1	360	1	CKR2_MACMU	O18793 macaca mula
2	1651.5	86.9	374	1	CKR2_HUMAN	P41597 homo sapien
3	1542	81.2	373	1	CKR2_RAT	O55193 rattus norv
4	1535	80.8	373	1	CKR2_MOUSE	P51683 mus musculu
5	1535	80.8	373	2	BAC32793	Bac32793 mus muscu
6	1513	79.6	373	2	Q6YT42	Q6yt42 sus scrofa
7	1513	79.6	373	2	BAD12134	Bad12134 sus scrof
8	1513	79.6	373	2	BAD08648	Bad08648 sus scrof
9	1513	79.6	373	2	BAD08655	Bad08655 sus scrof
10	1396	73.5	354	1	CKR5_MOUSE	P51682 mus musculu
11	1392	73.3	352	2	Q95NC2	Q95nc2 callicebus
12	1386	72.9	354	1	CKR5_RAT	O08556 rattus norv
13	1383	72.8	352	2	Q6YT41	Q6yt41 sus scrofa
14	1383	72.8	352	2	BAD12135	Bad12135 sus scrof
15	1383	72.8	352	2	BAD08649	Bad08649 sus scrof

16	1383	72.8	352	2	BAD08656	Bad08656 sus scrof
17	1377	72.5	352	2	Q6WN96	Q6wn96 leontopithe
18	1377	72.5	352	2	AAQ20015	Aaq20015 leontopit
19	1376	72.4	352	1	CKR5_CERTO	O62743 cercocebus
20	1376	72.4	352	2	Q71RS2	Q71rs2 cercocebus
21	1376	72.4	352	2	AAK69684	Aak69684 cercocebu
22	1375	72.4	352	2	O77776	O77776 cercocebus
23	1375	72.4	352	2	Q8HZT9	Q8hzt9 saimiri sci
24	1375	72.4	352	2	Q9MZA0	Q9mza0 callithrix
25	1375	72.4	352	2	AAQ20010	Aaq20010 saimiri s
26	1375	72.4	352	2	AAQ20011	Aaq20011 callithri
27	1374	72.3	352	2	Q6WN98	Q6wn98 callithrix
28	1374	72.3	352	2	AAQ20012	Aaq20012 callithri
29	1374	72.3	352	2	AAQ20013	Aaq20013 callithri
30	1373	72.3	352	2	Q6WN93	Q6wn93 leontopithe
31	1373	72.3	352	2	Q95NE1	Q95nel cercocebus
32	1373	72.3	352	2	AAQ20018	Aaq20018 leontopit
33	1371	72.2	352	1	CKR5_HYLLE	O97883 hylobates 1
34	1371	72.2	352	2	Q6WN97	Q6wn97 cebuella py
35	1371	72.2	352	2	Q9XT12	Q9xt12 cercopithec
36	1371	72.2	352	2	Q95NC4	Q95nc4 ateles geof
37	1371	72.2	352	2	Q95NC9	Q95nc9 alouatta se
38	1371	72.2	352	2	AAQ20014	Aaq20014 cebuella
39	1370	72.1	352	1	CKR5_MACFA	P61814 macaca fasc
40	1370	72.1	352	1	CKR5_MACMU	P61813 macaca mula
41	1370	72.1	352	1	CKR5_MACNE	P61815 macaca neme
42	1370	72.1	352	1	CKR5_PANPA	P60574 pan paniscu
43	1370	72.1	352	1	CKR5_PANTR	P56440 pan troglod
44	1370	72.1	352	1	CKR5_PONPA	P61756 pongo pygma
45	1370	72.1	352	1	CKR5_PONPY	O97881 pongo pygma

ALIGNMENTS

RESULT 1

CKR2_MACMU

ID CKR2_MACMU STANDARD; PRT; 360 AA.
 AC O18793;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN Name=CCR2; Synonyms=CMKBR2;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684; DOI=10.1089/088922201750290104;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).

CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC IsoId=O18793-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=O18793-2; Sequence=Not described;
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC -----

DR EMBL; AF013958; AAD11572.1; -.
 DR InterPro; IPR002237; CC_2_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
 KW Sulfation; Transmembrane.

FT	DOMAIN	1	42	Extracellular (Potential).
FT	TRANSMEM	43	70	1 (Potential).
FT	DOMAIN	71	80	Cytoplasmic (Potential).
FT	TRANSMEM	81	100	2 (Potential).
FT	DOMAIN	101	114	Extracellular (Potential).
FT	TRANSMEM	115	136	3 (Potential).
FT	DOMAIN	137	153	Cytoplasmic (Potential).
FT	TRANSMEM	154	178	4 (Potential).
FT	DOMAIN	179	206	Extracellular (Potential).
FT	TRANSMEM	207	226	5 (Potential).
FT	DOMAIN	227	243	Cytoplasmic (Potential).
FT	TRANSMEM	244	268	6 (Potential).
FT	DOMAIN	269	285	Extracellular (Potential).
FT	TRANSMEM	286	309	7 (Potential).
FT	DOMAIN	310	360	Cytoplasmic (Potential).
FT	CARBOHYD	14	14	N-linked (GlcNAc. . .) (Potential).
FT	MOD_RES	26	26	Sulfotyrosine (By similarity).
FT	DISULFID	113	190	By similarity.
SQ	SEQUENCE	360 AA;	41139 MW;	4B2552BCE913FE9F CRC64;

Query Match 97.1%; Score 1845; DB 1; Length 360;
 Best Local Similarity 96.9%; Pred. No. 5e-106;
 Matches 349; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	1	MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60

RT chemoattractant protein 1 receptor gene. Evidence for the role of the
 RT carboxyl-terminal tail in receptor trafficking.";
 RL J. Biol. Chem. 272:1038-1045(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
 RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
 RA Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
 RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
 RA Sagripanti J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
 RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.
 RX MEDLINE=20501139; PubMed=11046064;
 RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
 RA Chakravarty L., Kolattukudy P.E.;
 RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
 RT has tyrosine sulfation in a conserved extracellular N-terminal
 RT region.";
 RL J. Immunol. 165:5295-5303(2000).
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=A;
 CC IsoId=P41597-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P41597-2; Sequence=VSP_001893;
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; U03882; AAA19119.1; -.
 DR EMBL; U03905; AAA19120.1; -.
 DR EMBL; D29984; BAA06253.1; -.
 DR EMBL; U80924; AAC51637.1; -.
 DR EMBL; U80924; AAC51636.1; -.
 DR EMBL; U95626; AAB57791.1; -.
 DR EMBL; U95626; AAB57792.1; -.

DR EMBL; AF545480; AAN16400.1; -.
 DR PIR; I38450; I38450.
 DR PIR; JC2443; JC2443.
 DR PDB; 1KAD; Model; A=1-349.
 DR PDB; 1KP1; Model; A=1-349.
 DR Genew; HGNC:1603; CCR2.
 DR MIM; 601267; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.
 DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
 DR GO; GO:0006968; P:cellular defense response; TAS.
 DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
 DR GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.
 DR InterPro; IPR002237; CC_2_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW 3D-structure; Alternative splicing; G-protein coupled receptor;
 KW Glycoprotein; Polymorphism; Sulfation; Transmembrane.
 FT DOMAIN 1 42 Extracellular (Potential).
 FT TRANSMEM 43 70 1 (Potential).
 FT DOMAIN 71 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 100 2 (Potential).
 FT DOMAIN 101 114 Extracellular (Potential).
 FT TRANSMEM 115 136 3 (Potential).
 FT DOMAIN 137 153 Cytoplasmic (Potential).
 FT TRANSMEM 154 178 4 (Potential).
 FT DOMAIN 179 206 Extracellular (Potential).
 FT TRANSMEM 207 226 5 (Potential).
 FT DOMAIN 227 243 Cytoplasmic (Potential).
 FT TRANSMEM 244 268 6 (Potential).
 FT DOMAIN 269 285 Extracellular (Potential).
 FT TRANSMEM 286 309 7 (Potential).
 FT DOMAIN 310 374 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT MOD_RES 26 26 Sulfotyrosine.
 FT DISULFID 113 190 By similarity.
 FT VARSPLIC 314 374 SLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGR
 FT GKKGKSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRECK
 FT QCPVFYRETVDGVTSTNTPSTGEQEVSAAGL (in
 FT isoform B).
 FT /FTId=VSP_001893.
 FT VARIANT 64 64 V -> I (in dbSNP:1799864).
 FT /FTId=VAR_014339.
 FT VARIANT 355 355 G -> E.
 FT /FTId=VAR_014340.
 SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;

Query Match 86.9%; Score 1651.5; DB 1; Length 374;
 Best Local Similarity 95.5%; Pred. No. 4.2e-94;

Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

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Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      |||
Db      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      |||
Db     61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      |||
Db    121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
      |||
Db    181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      |||
Db    241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy    301 NPIIYAFVGEKFRRLSVFFRKHITKRFCKQCPV 334
      |||
Db    301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

```

RESULT 3

CKR2_RAT

```

ID   CKR2_RAT          STANDARD;          PRT;   373 AA.
AC   O55193;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2).
GN   Name=Ccr2; Synonyms=Cmkbr2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=98318173; PubMed=9655467;
RA   Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA   deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT   "Chemokine receptor expression in cultured glia and rat experimental
RT   allergic encephalomyelitis.";
RL   J. Neuroimmunol. 86:1-12(1998).
CC   -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC   chemokines. Transduces a signal by increasing the intracellular
CC   calcium ions level (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC   macrophages.
CC   -!- INDUCTION: In animals in which experimental allergic
CC   encephalomyelitis (EAE) has been induced.

```


CC -- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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DR EMBL; U77349; AAC03242.1; -.
DR RGD; 620876; Ccr2.
DR InterPro; IPR002237; CC_2_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 60 Extracellular (Potential).
FT TRANSMEM 61 81 Potential.
FT DOMAIN 82 91 Cytoplasmic (Potential).
FT TRANSMEM 92 112 Potential.
FT DOMAIN 113 128 Extracellular (Potential).
FT TRANSMEM 129 149 Potential.
FT DOMAIN 150 170 Cytoplasmic (Potential).
FT TRANSMEM 171 191 Potential.
FT DOMAIN 192 220 Extracellular (Potential).
FT TRANSMEM 221 241 Potential.
FT DOMAIN 242 256 Cytoplasmic (Potential).
FT TRANSMEM 257 277 Potential.
FT DOMAIN 278 301 Extracellular (Potential).
FT TRANSMEM 302 322 Potential.
FT DOMAIN 323 373 Cytoplasmic (Potential).
FT DISULFID 126 203 By similarity.
SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 81.2%; Score 1542; DB 1; Length 373;

Best Local Similarity 80.0%; Pred. No. 2.3e-87;

Matches 288; Conservative 24; Mismatches 48; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
 :||||| | | | : | | | | :||| | |||| | |||| :||||||| | | | | |
Db 14 ILSTSHSLFPRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73

Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 |||:|:|:|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74 MLVVIILISCKKLKSMTDIYLFNLAISDLLFLLTLPLFWAHYAANEWVFGNIMCKLFTGLY 133

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVAVFASLPGIIFTK 193

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
 : || | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 194 SEQEDDQHTCGPYFPTIWKNFQTIMRNILSLILPLLVMVICYSGILHTLFCRNEKKRHR 253

Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
		:: : : :	
Db	254	AVRLIFAIMIVYFLFWTPYNIVLFLTTFQEFLGMSNCVVDMLHDQAMQVTETLGMTHCCV	313
Qy	301	NPIIYAFVGEKFRRLYSVFFRKHITKRFCQKQCPVFYRETVDGVTSTNTPSTGEQEVSA	360
		: :	
Db	314	NPIIYAFVGEKFRRLYSIFFRKHIAKNLCKQCPVFYRETADRVSSFTPTSTGEQEVSVGL	373

RESULT 4

CKR2 MOUSE

```

ID   CCR2_MOUSE STANDARD; PRT; 373 AA.
AC   P51683; Q61172;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
DE   (JE/FIC receptor) (MCP-1 receptor).
GN   Name=Ccr2; Synonyms=Cmkbr2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96205938; PubMed=8631787;
RA   Boring L., Gosling J., Monteclaro F.S., Lulis A.J., Tsou C.-L.,
RA   Charo I.F.;
RT   "Molecular cloning and functional expression of murine JE (monocyte
RT   chemoattractant protein 1) and murine macrophage inflammatory protein
RT   1alpha receptors: evidence for two closely linked C-C chemokine
RT   receptors on chromosome 9.";
RL   J. Biol. Chem. 271:7551-7558(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=96216064; PubMed=8662823;
RA   Kurihara T., Bravo R.;
RT   "Cloning and functional expression of mCCR2, a murine receptor for the
RT   C-C chemokines JE and FIC.";
RL   J. Biol. Chem. 271:11603-11606(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97026720; PubMed=8872898;
RA   Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RA   Post T.W., Gerard C., Dorf M.E.;
RT   "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
RT   transcriptase-polymerase chain reaction does not detect mRNA for the
RT   KC or new MCP-1 receptor.";
RL   J. Neurosci. Res. 45:382-391(1996).
CC   -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC   chemokines. Transduces a signal by increasing the intracellular
CC   calcium ions level.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC   but not in nonhematopoietic cell lines.

```

```

CC      -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U47035; AAC52453.1; -.
DR      EMBL; U51717; AAC52557.1; -.
DR      EMBL; U56819; AAC52784.1; -.
DR      MGD; MGI:106185; Ccr2.
DR      GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR      GO; GO:0019955; F:cytokine binding; IPI.
DR      GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
DR      GO; GO:0030097; P:hemopoiesis; IMP.
DR      GO; GO:0006959; P:humoral immune response; IMP.
DR      GO; GO:0006954; P:inflammatory response; IMP.
DR      GO; GO:0019233; P:perception of pain; IMP.
DR      GO; GO:0030334; P:regulation of cell migration; IMP.
DR      InterPro; IPR002237; CC_2_receptor.
DR      InterPro; IPR000355; Chmkine_receptor.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRRHODOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane.
FT      DOMAIN      1      55      Extracellular (Potential).
FT      TRANSMEM     56      83      1 (Potential).
FT      DOMAIN      84      93      Cytoplasmic (Potential).
FT      TRANSMEM     94     114      2 (Potential).
FT      DOMAIN     115     127      Extracellular (Potential).
FT      TRANSMEM    128     149      3 (Potential).
FT      DOMAIN     150     166      Cytoplasmic (Potential).
FT      TRANSMEM    167     191      4 (Potential).
FT      DOMAIN     192     219      Extracellular (Potential).
FT      TRANSMEM    220     239      5 (Potential).
FT      DOMAIN     240     256      Cytoplasmic (Potential).
FT      TRANSMEM    257     281      6 (Potential).
FT      DOMAIN     282     298      Extracellular (Potential).
FT      TRANSMEM    299     322      7 (Potential).
FT      DOMAIN     323     373      Cytoplasmic (Potential).
FT      DISULFID     126     203      By similarity.
FT      CONFLICT      39      39      Y -> H (in Ref. 1).
FT      CONFLICT     184     184      A -> G (in Ref. 1).
FT      CONFLICT     264     264      V -> G (in Ref. 1).
SQ      SEQUENCE    373 AA; 42782 MW; FA012C10F4C9325A CRC64;

```

```

Query Match      80.8%; Score 1535; DB 1; Length 373;
Best Local Similarity 79.7%; Pred. No. 6.1e-87;
Matches 287; Conservative 25; Mismatches 48; Indels 0; Gaps 0;

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```

Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      :|||| | | |: | | :||| | |||| ||||| :|||||||

```

Db 14 ILSTSHSLFTRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73
 Qy 61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 |||::||| |||| :|||||||:|||| ||| ||||| |||:||||
 Db 74 MLVIIIIGCKKLKSMTDIYLLNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKVFTGLY 133
 Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 |||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVAVFASLPGIIFTK 193
 Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLRCRNEKKRHR 240
 ::|| | |||| : | || ||||| |:||||:||||| || |||||
 Db 194 SKQDDHHYTCGPYFTQLWKNFQTIMRNILSLILPLVMVICYSGILHTLFRCRNEKKRHR 253
 Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 |||:|| |||||:| |||| |:||| ||| |||||
 Db 254 AVRLIFAIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDKHLDQAMQVTETLGMTHCCI 313
 Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
 ||:|||||||:||||| || ||||| ||| |:|| ||||| ||
 Db 314 NPVIYAFVGEKFRRYLSIFFRKHIAKRLCKQCPVFYRETADRVSSTFTPSTGEQEVSVGL 373

RESULT 5

BAC32793

ID BAC32793 PRELIMINARY; PRT; 373 AA.
 AC BAC32793;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE 4 days neonate male adipose cDNA, RIKEN full-length enriched library,
 DE clone:B430108F19 product:chemokine (C-C) receptor 2, full insert
 DE sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Adipose;
 RX MEDLINE=99279253; PubMed=10349636;

Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 |||:|||||:|||||:|||||:|||||
 Db 134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVAVFASLPGIIFTK 193

Qy 181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHR 240
 :::| | |||| : | || ||||| :|||:||||| | | |||||
 Db 194 SKQDDHHYTCGPYFTQLWKNFQTIMRNILSLILPLLVMVICYSGILHTLFRCRNEKKRHR 253

Qy 241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
 |||:|| |||||:| |||| |:|| |||| |||||
 Db 254 AVRILFAIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDKHLDDQAMQVTETLGMTHCCI 313

Qy 301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGQEVSAGL 360
 ||:|||||:||||| || ||||| | :|| ||||| ||
 Db 314 NPVIYAFVGEKFRRYLSIFFRKHIAKRLCKQCPVFYRETADRVSSSTFTPTSTGQEVSAGL 373

RESULT 6

Q6YT42

ID Q6YT42 PRELIMINARY; PRT; 373 AA.
 AC Q6YT42;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Chemokine (C-C motif) receptor 2 (Chemokine C-C motif receptor
 DE 2).
 GN Name=CCR2;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
 RA Uenishi H.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AP006185; BAD08648.1; -.
 DR EMBL; AP006435; BAD08655.1; -.
 DR EMBL; AB119271; BAD12134.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR002237; CC_2_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

SO SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Best Local Similarity 78.9%; Pred. No. 1.4e-85;

Matches 284; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

Qy	1	MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN	60
Db	14	VLPTSHSLLTMNIGKNDDEPTTSYDYDYSEPCQKTSVGQIEALLPPLYSLVFIFGFVGN	73
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
Db	74	LLVVLILINCKKLKSMTDIYLLNLAI SDLLFLFTIPFWAHYAADQWVFGNIMCKFFTGLY	133
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTK	180
Db	134	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSGVTWVVAIFASLPGIIFIR	193
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR	240
Db	194	SQEEHSGYACAPYFPLAWKNFHTIMRSILGLVLPLLVMVVCYSGILKTLLRCRNEKKKKH	253
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
Db	254	AVRLIFVIMIVYFLFWAPYNIVLLLSTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI	313
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCQKQCPVIFYRETVDGVTSTNTPSTGEQEVSA	360
Db	314	NPIIYAFVGEKFRRYLSVFFRKHIAKHLCKQCPVIFYGETGDRMSSTYTPSTGEQEVSA	373

BAD12134

ID BAD12134 PRELIMINARY; PRT; 373 AA.

AC BAD12134;

DT 03-MAR-2004 (TrEMBLrel. 27, Created)

DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Chemokine C-C motif receptor 2.

GN CCR2.

OS Sus scrofa (Piq).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI TaxID=9823;

RN ...[1]

RP SEQUENCE FROM N.A.

RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,

RA Uenishi H.;

RT "Analysis of genomic structure of porcine CC chemokine receptor genes
RT and their expression.";

RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB119271; BAD12134.1; -.

KW Receptor.

SQ SEQUENCE 373 AA: 42299 MW: FA8E55CA527A34E0 CRC64:

Query Match 79.6%; Score 1513; DB 2; Length 373;

Best Local Similarity 78.9%; Pred. No. 1.4e-85;
Matches 284; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      :| || |   |   : || || :||| || |   |   |   |||||
Db      14 VLPTSHSLTMNIKGNDEEPTTSYDYDYSEPCQKTSVGQIEALLPPLYSLVFIFGFVGN 73

Qy      61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
      :||| ||||| :||| ||||| ||| :| || | ||| :||| ||| |||||
Db      74 LLVVLILINCKKLKSMTDIYLLNLAISDLLFLFTIPFWAHYAADQWVFGNIMCKFFTGLY 133

Qy     121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| :||| :||| :||| :||| :
Db     134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSGVTWVVAIFASLPGIIFIR 193

Qy     181 CQKEDSVYVCGPYFPRGWNNEFHTIMRNILGLVLPPLIMVICYSGILKTLLRCRNEKKRHR 240
      |:| | | | |||| | ||||| :||| ||||| :||| :||| ||||| ||||| :|:
Db     194 SQEEHSGYACAPYFPLAWKNFHTIMRSILGLVLPPLVMVVCYSGILKTLLRCRNEKKKKHK 253

Qy     241 AVRVIPTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
      ||| :|| ||||| ||||| :||| ||||| :||| :||| ||||| ||||| :|||
Db     254 AVRLIFVIMIVYFLFWAPYNIVLLSTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI 313

Qy     301 NPIIYAFVGEKFRRYLSVFFRKHITKRECKQCPVFYRETVDGVTSTNTPSTGEQEVSAGL 360
      ||||| ||||| ||||| | ||||| || | :|| ||||| ||||| |
Db     314 NPIIYAFVGEKFRRYLSVFFRKHIAKHLCKQCPVFYGETGDRMSSTYTPSTGEQEVSAAL 373
```

RESULT 8

BAD08648

ID BAD08648 PRELIMINARY; PRT; 373 AA.
AC BAD08648;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 2.
GN CCR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RT "Cloning of porcine CC chemokine receptor genes and clustering
RT structure on SSC13.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP006185; BAD08648.1; -.
KW Receptor.
SQ SEQUENCE 373 AA; 42299 MW; FA8E55CA527A34E0 CRC64;

Query Match 79.6%; Score 1513; DB 2; Length 373;
Best Local Similarity 78.9%; Pred. No. 1.4e-85;
Matches 284; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

```
Qy      1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
      :| || |   |   : || || :||| || |   |   |   |||||
```


Db	14	VLPTSHSLLTMNIGKNDEEPTTSYDYDYSEPCQKTSVGQIEALLLPPLYSLVFIFGFVGN	73
Qy	61	MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY	120
		: : : :	
Db	74	LLVVLILINCKKLKSMTDIYLLNLAI SDLLFLTIPFWAHYAADQWVFGNIMCKFFTGLY	133
Qy	121	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVT SVITWLVAVFASVPGIIFTK	180
		: : : : : : :	
Db	134	HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSGVTWVVAIFASLPGIIFIR	193
Qy	181	CQKEDSVYVCGPYFPRGWNNFHTIMRNLGLVLP LLIMVICYSGILKTLRLCRNEKKRHR	240
		: : : : : : : : : : : : : : : : : :	
Db	194	SQEEHSGYACAPYFPLAWKNFHTIMRSILGLVLP LLVMVVCYSGILKTLRLCRNEKKKHK	253
Qy	241	AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI	300
		: : : : : : : :	
Db	254	AVRLIFVIMIVYFLFWAPYNIVLLLSTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI	313
Qy	301	NPIIYAFVGEKFRRYLSVFFRKHITKRFCQKCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
		:	
Db	314	NPIIYAFVGEKFRRYLSVFFRKHIAHLCKQKCPVFYGETGDRMSSTYTPSTGEQEVSAAL	373

BAD08655

```

ID     BAD08655          PRELIMINARY;          PRT;    373 AA.
AC     BAD08655;
DT     02-MAR-2004 (TrEMBLrel. 27, Created)
DT     02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT     02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE     Chemokine (C-C motif) receptor 2.
GN     CCR2.
OS     Sus scrofa (Pig).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX     NCBI_TaxID=9823;
RN     [1]
RP     SEQUENCE FROM N.A.
RA     Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RT     "Cloning of porcine CC chemokine receptor genes and clustering
RT     structure on SSC13.";
RL     Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR     EMBL; AP006435; BAD08655.1; -.
KW     Receptor.
SQ     SEQUENCE    373 AA;  42299 MW;  FA8E55CA527A34E0 CRC64;

```

[illegible]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=97404635; PubMed=9261347;
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human
 RT immunodeficiency virus type 1.";
 RL J. Virol. 71:6305-6314(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Guo B., Kuno K., Harada A., Matsushima K.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
 CC but not in nonhematopoietic cell lines.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U47036; AAC52454.1; -.
 DR EMBL; X94151; CAA63867.1; -.
 DR EMBL; U68565; AAB37273.1; -.
 DR EMBL; U83327; AAC53386.1; -.
 DR EMBL; AF022990; AAC53389.1; -.
 DR EMBL; AF019772; AAB71183.1; -.
 DR EMBL; D83648; BAA12024.1; -.
 DR MGD; MGI:107182; Ccr5.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA...
 DR GO; GO:0006952; P:defense response; IMP.
 DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
 FT DOMAIN 1 32 Extracellular (Potential).
 FT TRANSMEM 33 60 1 (Potential).

Qy 311 KFRRLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
 ||| ||||| |||||:|:|::|:| |||| |||| ||
 Db 305 KFRSYLSVFFRKHIVKRFCKRCSIFQQDNPDRVSSVYTRSTGEHEVSTGL 354

RESULT 11

Q95NC2

ID Q95NC2 PRELIMINARY; PRT; 352 AA.
 AC Q95NC2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE C-C chemokine receptor 5.
 GN Name=CCR5;
 OS Callicebus moloch (Dusky titi).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;
 OC Callicebus.
 OX NCBI_TaxID=9523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF177887; AAK43370.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;

Query Match 73.3%; Score 1392; DB 2; Length 352;
 Best Local Similarity 75.4%; Pred. No. 3.7e-78;
 Matches 263; Conservative 30; Mismatches 50; Indels 6; Gaps 2;

Qy 18 EEVTTFFDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC 75
 | : :| |||| || | ||||:|||||||:|:|:|||||||:|:|
 Db 4 EVSSPIYDIDYGASEPCQKIDVKQMGALLPPLYSMVFLFGFVGNMLVVLILINCKRLKS 63
 Qy 76 LTDIYLLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFFIILLT 135
 :||||||| || ||:| ||| || :| ||| ||: |||| ||: |||||
 Db 64 MTDIYLLNLAISDLFFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLT 123

Qy	136	IDRYLAIVHAVFALKARTVTFGVVT	SVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP	195
			: : : :	
Db	124	IDRYLAIVHAVFALKARTVTFGVVT	SVITWVAVFASLPGIIFTRSQKEGYHYTCSPHFP	183
Qy	196	RG----	WNNFHTIMRNLGLVLP	251
		:	: : :	
Db	184	FGQYRFWKNLETLKMVILGLVLP	LLVMVICYSGILKTL	243
			LLRCRNEKKRHRAVRLIFTIMIV	
Qy	252	YFLEWTPYNIVILLNTFQEFFGLS	NCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK	311
			: : : ::	
Db	244	YFLEWAPYNIVLLLNTYQEFFGLN	NCCSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEK	303
Qy	312	FRRYLSVFFRKHITKRFCKQCPV	FYRETVDGVTSTNTPSTGEQEVSAGL	360
		:	: : : :	
Db	304	FRNYLLVEFFOKHIAKRFCKCCS	IFOKEAPERANSVYTRSTGEOEISVGL	352

CKR5 RAT

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ID   CKR5_RAT          STANDARD;          PRT;          354 AA.
AC   O08556;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
DE   alpha receptor).
GN   Name=Ccr5; Synonyms=Cmkbr5;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=98334064; PubMed=9670989;
RA   Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
RA   Berger M., Gebicke-Haerter P.J.;
RT   "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
RT   upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
RL   J. Neurosci. Res. 53:16-28(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=98318173; PubMed=9655467;
RA   Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA   Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT   "Chemokine receptor expression in cultured glia and rat experimental
RT   allergic encephalomyelitis.";
RL   J. Neuroimmunol. 86:1-12(1998).
CC   -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC   MIP-1-beta and RANTES and subsequently transduces a signal by
CC   increasing the intracellular calcium ions level.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation

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CC -----

DR EMBL; Y12009; CAA72737.1; -.
DR EMBL; U77350; AAC03243.1; -.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chm_kine_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 32 Extracellular (Potential).
FT TRANSMEM 33 60 1 (Potential).
FT DOMAIN 61 70 Cytoplasmic (Potential).
FT TRANSMEM 71 91 2 (Potential).
FT DOMAIN 92 104 Extracellular (Potential).
FT TRANSMEM 105 126 3 (Potential).
FT DOMAIN 127 143 Cytoplasmic (Potential).
FT TRANSMEM 144 168 4 (Potential).
FT DOMAIN 169 200 Extracellular (Potential).
FT TRANSMEM 201 220 5 (Potential).
FT DOMAIN 221 237 Cytoplasmic (Potential).
FT TRANSMEM 238 262 6 (Potential).
FT DOMAIN 263 279 Extracellular (Potential).
FT TRANSMEM 280 303 7 (Potential).
FT DOMAIN 304 354 Cytoplasmic (Potential).
FT DISULFID 103 180 By similarity.
FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 72.9%; Score 1386; DB 1; Length 354;
Best Local Similarity 74.9%; Pred. No. 8.7e-78;
Matches 262; Conservative 30; Mismatches 52; Indels 6; Gaps 2;

Qy 17 GEEVTTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLK 74
| | :| || ||| | :||| ||||| :| ||||:||||
Db 5 GSIPTYIDIDYSMSAPCQKVNKQIAAQLLPPLYSLVFIFGFVGNMVFLLILISCKKLK 64

Qy 75 CLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILL 134
:||||| ||||| :|| || ||||| ||||| :||| |||||
Db 65 SMTDIYLFNLAISDLLFLLTLPLFWAHYAANEWVFGNIMCKLFTGLIYHIGYFGGIFFIILL 124

Qy 135 TIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYF 194
||||| :||| ||| :||| :||| ||| : ||| ||| :|
Db 125 TIDRYLAIVHAVFAIKARTVNFVGVTSVVTWVAVFVSLPEIIFMRSQKEGSHYTCSPHF 184

Qy 195 ----PRGWNNFHTIMRNILGLVLP LLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMI 250
| | :| | : || :||| :||| || ||||| :|| |||
Db 185 LHIQYRFWKHFQTLKMWILSLPLLMVICYSGILNTLFRCRNEKKRHRAVRLIFAIMI 244

Qy 251 VYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGE 310
||||| :|| |||| :||| :||| :||| ||||| :|| :||| |||

Db 245 VYFLFWTPYNIVLLLTTFQEYFGLNNCSSNRLDQAMQVTETLGMTHCCLNPVIYAFVGE 304

Qy 311 KFRRLSVFFRKHITKRFCKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL 360
 ||| ||||| ||||| | : | : | | : | | ||||| ||

Db 305 KFRNYLSVFFRKHIVKRFCKHCSIFQQVNPDRVSSVYTRSTGEQEVSTGL 354

RESULT 13

Q6YT41

ID Q6YT41 PRELIMINARY; PRT; 352 AA.
 AC Q6YT41;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Chemokine (C-C motif) receptor 5 (Chemokine C-C motif eceptor 5).
 GN Name=CCR5;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
 RA Uenishi H.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AP006185; BAD08649.1; -.
 DR EMBL; AP006435; BAD08656.1; -.
 DR EMBL; AB119272; BAD12135.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Chmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHMOKINER.
 DR PRINTS; PR01110; CHEMOKINER5..
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40227 MW; 7464CB930911C987 CRC64;

Query Match 72.8%; Score 1383; DB 2; Length 352;
 Best Local Similarity 74.5%; Pred. No. 1.3e-77;
 Matches 260; Conservative 33; Mismatches 50; Indels 6; Gaps 2;

Qy	18	EEVTTFFDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC	75
Db	4	QTTSPFYDIDYGMSEPCQKTNRQIAARLLPPLYSLVFIFGFVGNLLVVLILINCKKLKS	63
Qy	76	LTDIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIIFFIILLT	135
Db	64	MTDIYLLNLAISDLLFLFTIPFWAHYAADQWVFGNTMCQFLTGFYFIGFFSGIIFIILLT	123
Qy	136	IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP	195
Db	124	IDRYLAIVHAVFALKARTVTFGVVTSGVTWVVAIFASLPGIIFTKSQKEGSRYTCSPHFP	183
Qy	196	RG----WNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIV	251
Db	184	SSQYHFWKNFQTLKMVILGLVLP LLVMVVCYSGILKTLRLCRNEKKKKHKAURLIFAIMIV	243
Qy	252	YFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK	311
Db	244	YFLEWAPYNIVLLLSTFQEFFGLNNCSGSNRLDQAMQVTETLGMTHCCINPIIYAFVGEK	303
Qy	312	FRRYLSVFFRKHITKRFECKQCPVFYRETVDGVTSTNTPSTGEQEVSAAGL	360
Db	304	FRSYLLGFFRKHIVRRFECKGCPVFOAEAPDRVSSVYTRSTGEOEISVGL	352

BAD12135

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ID      BAD12135      PRELIMINARY;      PRT;      352 AA.
AC      BAD12135;
DT      03-MAR-2004 (TrEMBLrel. 27, Created)
DT      03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT      03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE      Chemokine C-C motif eceptor 5.
GN      CCR5.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
RA      Uenishi H.;
RT      "Analysis of genomic structure of porcine CC chemokine receptor genes
RT      and their expression.";
RL      Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AB119272; BAD12135.1; -.
SQ      SEQUENCE      352 AA;  40227 MW;  7464CB930911C987 CRC64;
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Qy 18 EEVTTTFDYYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNNMLVVLILINCKKLKC 75
: : |:| || | | :|| |:|||||||||||||||:|||||||||||
Db 4 QTTSPPFYDIDYGMSEPCQKTNRQIAARLLPPLYSLVFIFGFVGNNLLVVLILINCKKLKS 63

Qy 76 LTDIYLLNLAISDLLFLITLPIWAHSAANEWVFNGAMCKLFTGLYHIGYFGGIFFIILLT 135

```

      :||||| :| ||| ||::||| ||: || | ||:| |||||
Db      64 MTDIYLLNLAIISDLLFLFTIPFWAHYAADQWVFGNTMCQFLTGFYFIGFFSGIFFIILLT 123
Qy      136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
      ||||| :||:|:|:|:| ||| | | | |:|
Db      124 IDRYLAIVHAVFALKARTVTFGVVTSGVTWVVAIFASLPGIIFTKSQKEGSRYTCSPHFP 183
Qy      196 RG----WNNFHTIMRNILGLVLP LLIMVICYSGILKTL LRCRNEKKRHRAVRVIFTIMIV 251
      | || |: |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      184 SSQYHFWKNFQTLKMVILGLVLP LLVMVCYSGILKTL LRCRNEKKKKHKA VRLIFAIMIV 243
Qy      252 YFLEWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK 311
      ||||| ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      244 YFLEWAPYNIVLLLSTFQEFFGLNCSGNSRLDQAMQVTETLGMTHCCINPIIYAFVGEK 303
Qy      312 FRRYLSVFFRKHITKRFCQCPVFYRETVDGVTSTNTPSTGEQEV SAGL 360
      || || ||||| :||| ||| | | |:| | |||||:| ||
Db      304 FRSYLLGFRRKHIVRRFCKGCPVFQAEAPDRVSSVYTRSTGEQEISVGL 352

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RESULT 15

BAD08649

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ID      BAD08649      PRELIMINARY;      PRT;      352 AA.
AC      BAD08649;
DT      02-MAR-2004 (TrEMBLrel. 27, Created)
DT      02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT      02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE      Chemokine (C-C motif) receptor 5.
GN      CCR5.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RT      "Cloning of porcine CC chemokine receptor genes and clustering
RT      structure on SSC13.";
RL      Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AP006185; BAD08649.1; -.
KW      Receptor.
SQ      SEQUENCE      352 AA;      40227 MW;      7464CB930911C987 CRC64;

```

```

Query Match      72.8%;      Score 1383;      DB 2;      Length 352;
Best Local Similarity      74.5%;      Pred. No. 1.3e-77;
Matches 260;      Conservative 33;      Mismatches 50;      Indels 6;      Gaps 2;

```

```

Qy      18 EEVTTFDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC 75
      : : |:| || | |:| |:|||||:|||||
Db      4 QTTSFPYDIDYGMSEPCQKTNVRQIAARLLPPLYSLVFIFGFVGNLLVVLILINCKKLKS 63
Qy      76 LTDIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLT 135
      :||||| :| ||| ||::||| ||: || | ||:| |||||
Db      64 MTDIYLLNLAIISDLLFLFTIPFWAHYAADQWVFGNTMCQFLTGFYFIGFFSGIFFIILLT 123
Qy      136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
      ||||| :||:|:|:|:| ||| | | | |:|

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